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ASIJUL

ASIJUL

nef protein - human immunodeficiency virus type 1 (isolate LV)

Nylleranate names: 3'-orf protein; orf-F protein

C; Species: human immunodeficiency virus type 1, HIV-1

C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C; Accession: A40007

R; Muesing, M. A.; Smith, D. H.; Cabradilla, C. D.; Benton, C. V.; Lasky, L. A.; Capon, D.J

Nature 313, 450-458, 1985

A; Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr

A; Reference number: A93355; MUID:85111157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A04006
R;Arya, S.K.; Gallo, R.C.
R;Arya, S.K.; Gallo, R.C.
A;Title: Three novel genes of human T-1ymphotropic virus type III: immune reactivity
A;Reference number: A94093; MUID:86177573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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A;Cross-references: EMBL:M11840; NID:g328453; PIDN:AAA45001.1; PID:g328458
121 FPDXQNYTPGPGVRYPLTFGWCYKLVPVEPDKIEEANKGENTSLLHPVSLHGMDDPEREV 180
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A;Residues: 1-206 <MUE>
A;Cresicreferences: GB:K02083; NID:g555008; PIDN:AAB59874.1; PID:g328560
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.0%; Score 1114; DB 1; Length 206; 97.6%; Pred. No. 3.8e-85; ive 3; Mismatches 2; Indels
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Pred. No. 1.2e-84;
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                                            LEWRFDSRLAFHHVARELHPEYFKNC 206
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
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97.1%;
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Matches 201; Conservative
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C;Accession: S03244
S;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu A;Reference number: S03244; MUID:86067228
A;Reference number: S03244; MUID:86067228
A;Residues: 1-206 <RAT>
A;Residues: 1-206 <RAT>
A;Residues: 1-206 <RAT>
A;Residues: 1-206 <RAT>
A;Rotoser references: EMBL:X03187
A;Note: the in-frame stop codon at residue 124, shown as 'X', may be suppressed
                                                                                                                                                                                human immunodeficiency vi
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N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb.1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C;Accession: S03244
                                                          Species: human immunodeficiency virus type 1, HIV-1
Date: 20-oct-1994 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
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                                  nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-0ct-1994 #sequence_revision 10-Nov-1995 #text_change 03-C:Accession: S44467
R:Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
Eur. J. Blochem. 221, 811-819, 1994
A;Title: Stability and proteolytic domains of Nef protein from huma A;Reference number: S43467; MUID:94229079
A;Accession: S44467
A;Accession: S4467
A;Accession: S42467
A;Accession: S42467
A;Accession: S42467
C;Superfamily: AIDS nef protein
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Pred. No. 3.2e-85;
0; Mismatches 2;
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Pred. No. 3.2e-85;
2; Mismatches 1;
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Best Local Similarity 98.5%;
Matches 203; Conservative
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Best Local Similarity 99.0%;
Matches 203; Conservative
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Superfamily: AIDS nef protein
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August 26, 2002, 08:08:31; Search time 50.45 Seconds (without alignments) 575.203 Million cell updates/sec
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1688
1 MGCKWSKSSVVGWPTVRERM......QSRGDPTGPKETSGHHHHHH 302
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1040440001	nef protein - huma	f protein -	protein (c	protein -	f protein -	f protein -	protein (c	protein -	f protein -	f protein -	protein (c	profein	protein -	protein .	protein -	protein -	protein -	ns-activati	trans-activating t	trans-action t	nef protein - simi	protein -	protein	Processi	nef protein - simi				
SUMMARIES		ASLJFV	S43467	S03244	ASLJVL	ASLJ12	JC5400	503245	S33986	SLJH3	24985	ASLJBR	S25937	ASLJ02	I44001	503247	S03246	QQLJZR	OOLJND	B44963	T01673	ASLJIK	S33982	TNLJ12	A25700	S46353	S54385	T09446	44001	507993
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% Query Match		6.99	66.1	66.1	0.99	65.6	65.0	64.9	64.9	64.1	60.4	60.4	59.7	59.1	58.7	58.5	58.5	54.0	53.5	49.6	49.4	49.3	28.8	28.3	27.8	26.2	26.0	25.9	25.7	25.4
Score		1130	1115	1115	1114	1108	1097	1096	1096	1081.5	1019	1019	1007	997	991.5	987	987	911	903.5	837	834.5	832	486	478	470	443	439.5	437	434	429.5
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121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180 

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nef protein - simi nef protein - huma nef protein - huma nef protein - huma nef protein - simi transactivator pro nef protein - simi tat protein - simi trans-activating t trans-activating t nef protein - huma trans-activating t nef protein - huma nef protein - simi nef protein - simi nef protein - huma	ALIGNMENTS  virus type 1 (isolate LAV-la)  rf-F protein  rus type 1, HIV-1  on 17-May-1985 #text_change 16-Jul-1999  , O.; Cole, S.; Alizon, M.  AIDS virus, LAV.  99333  amrch 1991  March 1991  phosphoprotein	tch 66.9%; Score 1130; DB 1; Length 206; al Similarity 100.0%; Pred. No. 1.8e-86; 206; Conservative 0; Mismatches 6; Indels 0; Gaps 0; MGGKWSKSSVYGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
111567 853099 812160 ASLJCZ ASLJCZ 171556 171556 171556 171558 171578 854851 854861 ASLJCR ASLJCR ASLJCR ASLJCR 170669	ALIGNMENT  immunodeficiency virus ty  unodeficiency virus type unodeficiency virus type unodeficiency virus type fisquence_revision 17-May S14609 onigo, P.; Danos, O.; Col sequence of the AIDS viru A90866; MUID:85099333 AI> GB:K02013; NID:g326417; P e: isolate LAV-la L Data Library, March 199 S14607 IC> EMBL:X58780; NID:g60113; orf-F nef protein munodeficiency; phosphopry	Score 11 Pred. N O: Misme EPAADGVGA
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	an immunodeficiency vi: 3'-orf protein; orf: 1 manunodeficiency virus 1 sapiens (man) 108; \$14609 15 Sonigo, P.; Danos, O 16 Sequence_revision 16 Sonigo, P.; Danos, O 17 Sonigo, P.; Danos, O 18 Sonigo, NID:g6 18 Sonigo, NID:g6 18 Sonigo, NID:g6 18 Sonigo, O	66.9%; larity 100.0%; Conservative SSVGWPTVRERMRRA !!!!!!!!!!!!!
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nef protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S33986
R;Carlini, F.
B;Carlini, F.
B;Date Library, November 1991
A;Reference number: S33979
A;Accession: S33986
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Streicher,
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                            EMBL: X03188; NID: 961556; PIDN: CAA26947.1
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Pred. No. 1.2e-83;
3; Mismatches 4;
                                                                                                                                        Score 1096; DB 2;
Pred. No. 1.2e-83;
                                                                                                                                                                              Mismatches
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Best Local Similarity 96.6%;
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:211530;
C;Superfamily: AIDS nef protein
                                                                                                                                          64.9%;
96.6%;
                                                                                    protein
                                                                                                                                                                                  Conservative
                                                                A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAR>
                                                                                                                                                                Similarity
                              A; Cross-references:
C; Genetics:
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Best Local Simi
Matches 199;
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N.Alternate names: 3' orf protein

C;Species: human immunodeficiency virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999

C;Accession: S03245

R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa Nucleic Acids Res. 13, 8219-8229, 1985

Nucleic Acids Res. 13, 929-8259, 1985

A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acquare commber: S03244; MUID:86067228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     possesses membrane-perturbing and fusogenic activitie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to yeast
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C;Species: Human immunodeficiency virus type 1, HIV-1
C;Species: Human immunodeficiency virus type 1, HIV-1
C;Species: 07-Unl-1997 #sequence_revision 18-Jul-1997 #text_change 31-Oct-1997
C;Accession: JC5400
R;Macreadie, I.G.; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.
Biochem. Blophys. Res. Commun. 232, 707-111, 1997
A;Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides the Recence number: JC5400; MUID:97271389
A;Reference number: JC5400
A;Reference number: JC5400
A;Rocession: JC5400
A;Rocession: JC5400
C;Comment: The amino-terminal part possesses membrane-perturbing and fusogenic and comments.
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Pred. No 9.9e-84;
1; Mismatches 5;
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C;Superfamily: AIDS nef protein
F;2-206/Product: nef protein #status predicted <MAT>
                                    Mismatches
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Best Local Similarity 97.1%;
Matches 200; Conservative
                                      Conservative
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A; Molecule type: DNA
A; Residues: 1-206 <RAT>
                                    200;
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C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: 524965
R;Harits, M; Hislop, S; Patsilinacos, P; Neil; J.C.
Submitted to the EMBL Data Library, November 1991
A;Poscription: In vivo derived HIV-1 NEF genes are heterogeneous and lack detectable nucle A;Accession: 524985
A;Status: preliminary
A;Molecule type: DNA
A;Rossidues: 1-204 <HRR>
A;Cross-references: Pur-
C;Superfa-
           Dora
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R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Inberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F. Mature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123
A;Accession: A04005
A;Molecule type: DNA
A;Residues: 1-205 <RAT>
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; Immunodeficiency
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Pred. No. 1.9e-82;
4; Mismatches 3;
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60.4%; Score 1019; DB 2;
Best Local Similarity 89.8%; Pred. No. 2.9e-77;
Matches 185; Conservative 10; Mismatches 9;
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96.18;
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Best Local Similarity
Matches 198; Conserv
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A; Ross-references: GB:M21098; NID:9326426; PIDN:AAA44222.1; PID:9326431
A; Cross-references: GB:M21098; NID:9326426; PIDN:AAA44222.1; PID:9326431
B; Steuler, H; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A; Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid A; Reference number: $21990
A; Recession: $21993
A; Molecule type: DNA
A; Residues: 1-7 <STE>
N'Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1 (isolate BR)
A'Note: how Homo sapiens (man)
C:Date: 31-Dec-1989 Asequence_revision 131-Dec-1989 #text_change 16-Jul-1999
C:Accession: D31667; S21993; S21995; S21999; S21991
R:Anand, R: Thayer, R: Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; I
A'Title: Blological and molecular characterization of human immunodeficiency v
A'Reference number: A94389; MUID:89085613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:9584028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:g60182; PIDN:CAA43631.1; PID:g584030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1019; DB 1; Length 218; Pred. No. 3.1e-77; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:960179; PIDN:CAA43623.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:960181; PIDN:CAA43625.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 PVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X61356;
A; Accession: S21999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.4%;
Best Local Similarity 84.1%;
Matches 185; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA A; Residues: 1-7 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: E.
A.Accession: S21997
A.Molecule type: DNA
A.Residues: 1-7 <ST3>
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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A; Accession: $21995
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nef protein - human immunodeficiency virus type 1 (strain YU-2)
N;Alternate names: 3 -orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Feb-1997
C;Accession: I44001
F;Li, Y; Hui, H; Buxgess, C.J; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J; Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties
A;Reference number: A44001; MUID:93021387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)
N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28 Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Jun-2000
C;Accession: S03247
R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated w A;Reference number: S03244; MUID: 86067228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
A;Residues: 1-182 <RAT>
A;Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 INADCAMLEAQEEEEVGFPVRPQVPLRPMTHKAAMDLSHFLKEKGGLEGLIHSQQRQDIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DLWYXHTQGYFPDWQNYTPG-GTRWPLTFGWCFKLVPVEPEKIEEANAGENNCLLHPMSQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 VDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PAADGVGAVSRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLSPMTYKAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGGKWSKSSVVGWPTVR-----ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA
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Pred. No. 1.2e-74;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 991.5; DB 1
; Pred. No. 5.9e-75;
12; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKN 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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84.2%;
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ilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                     A;Accession: 144001
A;Molecule type: DNA
A;Residues: 1.214 <LIY>
A;Cross-references: GB:M93258
C;Genetics:
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Best Local Similarity
Matches 181; Conserva
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Best Local Similarity
Matches 179; Conserv
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S03247
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R; Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Si
Solience 227, 484-492, 1985
A; Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A; Reference number: A04003; MUID:85090453
A; Accession: A04009
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-210 <SAN>
A; Cross-references: GB: K02007; NID:9328658; PIDN:AAB59883.1; PID:9328667
A;Reference number: S25937; MUID:91156044
A;Accession: S25937
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: nucleic acid
A;Residues: 1-206 <GUO>
A;Cross-references: DMBL:X57465; NID:960217; PIDN:CAA40702.1; PID:960218
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C;Superfamily: AIDS nef protein
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N'Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                           ; Score 1007; DB 2;
; Pred. No. 2.9e-76;
18; Mismatches 11;
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Best Local Similarity 85.2%; Pred. No. 2e-75;
Matches 179; Conservative 16; Mismatches
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                59.7%;
85.9%;
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Length 214;

DB 1; 11; the virus associated with the a

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Length 182;

Livak, K.J.;

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Gaps

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Length 212;

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A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human im A;Reference number: JQ0065; MUID:90034200
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B44963
nef protein - human immunodeficiency virus type 1 (isolate Z321)
N.Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 *sequence_revision 17-Feb-1994 *text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Distriction - human immunodeficiency virus type 1 (isolate NDK)
N.Alternate names: 3'-orf protein; Orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo saplens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: JQ006B
C:Spire, B:: Sire, J:
C:Spire, B:: 
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                                                                                                                                                                                                                                                                            AWLEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:M27323; NID:g328154; PIDN:AAA44874.1; PID:g328163
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERM-----RRAEPAADGVGAASRDLEKHGAITSSNTAATNAAC
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                                                   Score 911; DB 1;
Pred. No. 2.8e-68;
; Mismatches 19
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                                                                                                            23;
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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ilarity 77.3%;
Conservative 2
                                                   54.0%;
larity 77.4%;
Conservative 2:
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Best Local Similarity
Matches 160; Conserva
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A; Residues: 1-207 <SPI>
                                                                                 Similarity
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                                                      Query Match
                                                                                       Best Loca
Matches
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A;Reference number: A26192; MUID:87248097
A;Accession: F26192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa
Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu
A;Reference number: S03244; MUID:86067228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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A;Residues: 1-212 <SRI>
A;Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45381.1; PID:g329404
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Superfamily: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.; Schochetman,
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N'Alternate names: 3'-orf protein, orf-F protein
C;Species: human immunodeficiency virus Zr-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C;Accession: F26192
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schoche Gene 52, 71-82, 1987
                                                                                                                                                                                                                                                                                                                                                                                            nef protein (clone HAT3) - human immunodeficiency virus type 1
N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Accession: S03246
QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 QEDEEVGFPVRPQVPLRPMTFKAAVDLSHFLKEKGGLDGLVFSQKRQDILDLMVYHTQGY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAA26949.1; PID:g61551 for residue 11 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HGENESKSKMSGWPAVRERMOKAEPAADGVGAASRDLEKHGTITSSNT--NNAACTWLEA
                                                                                    LVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYFK
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; Pred. No. 1.3e-74;
16; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X03190; NID:961550; A;Note: the authors translated the codon AGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEWRFDSRLAFHHVARELHPEYFKNC 206
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84.5%;
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C;Superfamily: AIDS nef protein
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Best Local Similarity 84.5%
Matches 174; Conservative
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A; Molecule type: DNA
A; Residues: 1-204 <RAT>
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NC 182
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F.; Hampe,

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Gaps

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Length 207;

120

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#text\_change 16-Jul-1999

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A) Cross-references: EMBL:211530; NID:960192; PIDN:CAA77625.1; PID:960196
R) Siderovski, D. P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Summer Nucleic Acids Res. 20, 5311-5320, 1992
A) Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activato A; Reference number: $26385; MUD:93065196
A) Reference resistance nucleic acid
A; Recession: $26385
A; Molecule type: nucleic acid
A; Residues: 1-86 <SID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipacies: human immunodeficiency virus type 1, HIV-1
Cipacies: human immunodeficiency virus type 1, HIV-1
Cipacies: human immunodeficiency virus type 1, HIV-1
Cipacies: 06-oct-1994 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
Cipaccession: S33982; S26385; S19864
RiCarlini, F. Submitted to the EMBL Data Library, November 1991
A;Recession: S33999
A;Accession: S33998
A;Molecule type: DNA
A;Residues: 1-86 <CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                        A,Accession: S09991
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-205 <HUE>
A,Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36408.1; PID:958877
C,Genetics:
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency
                                                                                        nef protein - simian immunodeficiency virus SIVepz
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: sinian immunodeficiency virus SIVepz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_C;Accession: S09991
E;Huet, T.: Cheynier, R.; Meyerhans, A.; Roelants, G.; Wa Nature 345, 366-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus
A;Reference number: S09983; MUID:90259077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1; L4
9.8e-62;
ches 34;
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C;Keywords: AIDS; immunodeficiency
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C;Superfamily: AIDS nef
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C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C; Accession: T01673
R; Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A; Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
A; Recession: T01673
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-209 <ALI>A; Cross-references: FMP:
C;Accession: B44963
K;Sinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A;Ittle: Molecular characterization of HIV-1 isolated from a serum collected in 1976: r A;Reference number: A44963; MVID:89228766
A;Reference number: A44963; MVID:8922876
A;Residues: 1-205 <SRI>A;Residues: 1-205 <SRI>A;Rocross: GB:M15896; NID:g329392; PIDN:AAB53951.1; PID:g329397
C;Genetics: A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Reywords: AIDS; immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                Length 205;
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                                                                                                                                                                                                                                                                                                                                                49.6%; Score 837; DB 1; 73.2%; Pred. No. 3.8e-62; iive 23; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EREVLEWRFDSRLAFHHVARELHPEYFKN 205
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 73.29
Matches 153; Conservative
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Gaps

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Length 205; Indels

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A,Molecule type: DNA
A,Residues: 1-226 <JIN>
A,Residues: 1-226 <JIN>
A,Cross-references: EMBL:U04005; NID:9466229; PIDN:AAA21511.1; PID:9466237
A,Experimental source: isolate SAB-1; sabaeus monkey
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1999
C,Genetics:
                                                                                                                                                                    C. Date: 25-Dec.1994 #sequence_revision 14-Feb-1997 #text_change 20-Sep-1999 C. Accession: $46353 # Sequence_revision 14-Feb-1997 #text_change 20-Sep-1999 C. Accession: $46353 # Sequence_revision 14. Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V. EMBO J. 13, 2935-2947, 1994 # Sequence of simian immunodeficiency virus from West African A; Reference number: $46335; MUID:94298785
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$54385

Cipatein - human immunodeficiency virus type 1 (fragment)
Cispecies: human immunodeficiency virus type 1, HIV-1
Cipate: 15-101-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
Cincession: S54885
Ritheodore, T.; Buckler-White, A.J.
Submitted to the BMBL Data Library, July 1989
A:Reference number: S54377
A:Reference number: S54385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 LIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:9329377; PIDN:AAA45371.1; PID:9555045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AATNAAC-----AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGGKWSKS----SVVGWPTVRER-MRRAEPAADGVGAASRDLE-----KHGAITSSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                        nef protein - simian immunodeficiency virus SIVagm (isolate SAB-1)
C;Species: simian immunodeficiency virus SIVagm
A;Variety: isolate SAB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                            A,Accession: $46353
A,Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 439.5; DB 2;
Pred. No. 1.6e-29;
6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 26.2%; Score 443; DB 2; L
Best Local Similarity 44.1%; Pred. No. 2.1e-29;
Matches 98; Conservative 30; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGG 96
86
  SQTHQVSLSKQPTSQPRGDPTGPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%;
ilarity 84.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A) Status: preliminary
A; Molecule type: genomic RNA
Residues: 1-97 CTHE>
A; Cross-references: EMBL: M22639;
C; Superfamily: AIDS nef protein
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C;Superfamily: AIDS nef protein
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Best Local Similarity
Matches 82; Conserv
62
                                                               RESULT
S46353
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Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of A; Accession: A04093; MUID:86177573
A:Accession: A04017
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                                                                                                                                                                                                                                                                                                                                                   trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate C.Species: human immunodeficiency virus type 1, HIV-1 A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
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                                                                                                        209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                  Gaps
                                                                                                                                 2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFIIKALGISYGRKKRQRRRPPQG 61
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R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, Science 239, 74-77, 1985
A;Reference number: A25700; WUD:85244627
A;Accession: A25700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 470; DB 2; Length 86;
Pred. No. 4.2e-32;
0; Mismatches 3; Indels
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                      Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: AIDS trans-activating transcription regulator Keywords: AIDS; immunodeficiency; transcription regulation
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Pred. No. 1e-32;
0; Mismatches 1.
                      Score 486; DB 2;
Pred. No. 2e-33;
                                  100.0%; Pred. ...
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                                                                                                                                                                                               269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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                                                                                                                                                                                                                      SOTHQVSLSKQPTSQSRGDPTGPKE 86
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98.8%;
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larity 96.5%;
Conservative (
                      28.88;
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Best Local Similarity
Matches 84; Conserv
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nes 82; Conserv
                                         Local Similarity
tes 85; Conserv
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A; Residues: 1-95 <ARY>
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A; Residues: 1-86 <SOD>
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Matches 82
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Matches
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C; Species: simian immunodeficiency virus SIVsm
A; Variety: strain E543
C; Accession: 111567
C; Accession: 111567
C; Atrol., V.M.; Adger-Johnson, D.; Cambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.
J. Virol., 71, 1608-1620, 1997
A; Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodefi
A; Reference number: 217285; MUID:97131152
                                                                                                                                             Ritizech, V.M.; Olmsted, R.A.; Murphey-Corb, M.; Purcell, R.H.; Johnson, P.R. Nature 319, 319-392, 1989
A; Title: An African primate lentivirus (SIV(sm)) closely related to HIV-2.
A; Reference number: S04237; MUID: 89262053
A; Accession: S07993
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: genomic RNA
A; Residues: 1-309 <HIR>
A; Cross-references: EMBL: X14307; NID: 961741; PIDN: CAA32488.1; PID: 961747
A; Note: this sequence was submitted to the EMBL Data Library, February 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1.259 <HIR>
A; Cross-references: EMBL:U72748; NID:g1695908; PIDN:AAC$6566.1; PID:g1695917
C; Genetics:
                                                                          C;Species: simian immunodeficiency virus SYVam
A;Note: host Cercocebus torquatus atys (sooty mangabey)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C;Accession: S07993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTSEPVDPRLE-----PWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGKWSKSSVVGWPTVRERMRRA------EPAADGVGAASRDL-----EKH 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 LSEEEVKRRLTARGLLKWLTRRKQAETAGT-----FH-----KGLSWEVLGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 GAITSSNTAATNAACAW-----LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 309;
                                                  simian immunodeficiency virus SIVsm (1solate F236)
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Pred. No. 4e-28;
4; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Mismatches
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.4%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: AIDS nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local Simi
Matches 106;
                                                     nef protein
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                c.c. protein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C;Accession: T09446
R;Pang, S;Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A;Reference number: 216673
A;Accession: T09446
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resdiues: preliminary; translated from GB/EMBL/DDBJ
A;Resdiues: 1-101 <PAN>
A;Cross-references: EMBL:U63632; NID:g1465777; PID:g1465783
A;Gene: tat
A;Introns: 72/2
C;Superfam*1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. J. Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties A;Reference number: A44001; MUID:93021387
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jul-1998
C;Accession: E44001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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A;Cross-references: GB:M93258
C;Genetics: A;Gene: tat
A;Gene: tat
A;Introns: 72/2
C;Superfamily: AIDS trans-activating transcription regulator C;Keywords: AIDS; immunodeficiency; transcription regulation
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87.2%; Pred. No. 4.9e-29;
tive 2; Mismatches 9;
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Pred. No. 2.7e-29;
2; Mismatches 8
269 SQTHQVSLSKQPTSQSRGDPTGPKET 294
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25.9%;
Best Local Similarity 88.4%;
Matches 76; Conservative
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Matches 75; Conservative
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•	Matches	Matches 97; Conservative 38; Mismatches 78; Indels 37; Gaps 6;
ογ		SVVGWPTVRERMRRAEPAADGVGAASRDL
QQ	-	MGGAISKKQYRRGGNLRERLLARARGETYGRLWEGLEEGYSQSLGASGRGLSSLSCEPQKY 60
Qy		41 GAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLS 88
qq		61 SEGQYMNTPWRNPTAEKAKLGYKQQNMDDVDDEDDDLVGVSVHPKVPLRAMTYKLAIDMS 120
δ		89 HPLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPV 148
qq	121	HEIKEKGGLEGIYYNEKRHRILDMYMEKEEGIIPDMQNYTLGPGTRYPMHFGWLWKLVPV 180
Qγ	149	ä
QQ		181 DVSDEAQEDETHCLVHPAQTHQMDDPWGEVLAWRFDPELAYSYRAFIKYPEEFGSKSG 238
δ		206 CTSEPVDPRL 215
q		339 LSEEEVKRRL 248

Search completed: August 26, 2002, 08:13:21 Job time: 290 sec

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Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' or fencodes a phosphorylated GTP-binding protein resembling
an oncogene product.";
Nature 330:266-269(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "FAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 54-205 IN COMPLEX WITH NEF. MEDLINE-96279837; PubMed-8681387;
Lee C.H., Saksela K., Mirza U.A., Chait B.T., Kurlyan J.;
Lee C.H., Satsela K., Mirza U.A., Chait B.T., Kurlyan J.;
"Crystal structure of the conserved core of HIV-1 Nef complexed with a Src family SH3 domain.";
cell BS:931-942(1996).
-1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
                                                          simian
                                                                  simian
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                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (BRU isolate) (HIV-1), and Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
        P19553
P35965
P05905
P19552
P12482
P12482
P17501
P1753
P04614
P20893
                                                                                                                                                                                                                                                                                                                                        Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.; "Nucleotide sequence of the AIDS virus, LAV."; Cell 40:9-17(1985).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (CLONE PNL4-3).
STRAIN-ISOLATE NEW YORK-5;
BUCKler C.E., Buckler-White A.J., Willey R.L., MCCOy J.;
Submitted (JUN-1988) to the EMBL/GenBank/JDBJ databases.
                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
                                                                                                                                                                                       206 AA
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         TAT_HVIS1
TAT_HVIY2
TAT_HVIMN
TAT_HVIS3
NEF_HV2KR
NEF_SIVS4
                                                                                     TAT_HV1A2
TAT_HV1OY
NEF_HV2BE
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MEDLINE-85099333; PubMed-2981635;
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Compugen Ltd
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         GenCore version
Copyright (c) 1993 - 2000
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NEF_HV1S3
NEF_HV1OY
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1108
11088.5
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us-09-509-239-13.rsp

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EMBL; U12055; AAA76691.1; -.
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                                                                                                                                                                                                                                                                     Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                         61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                     121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
                                                                                                                                                                                                                        1 MGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSVTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                    Nature 330:266-269(1987).
-1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
                                                                                                                                                                                                           MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
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Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                                                                       ö
                   InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.
                                                                                                                                                                Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11700;
                                                                                                                                                                                       indels
                                                                              V -> I. (IN CLONE PNL4-3).
T -> A (IN CLONE PNL4-3).
A -> V (IN CLONE PNL4-3).
T -> N (IN CLONE PNL4-3).
Y: 77453FC80B6004F2 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                    PHOSPHORYLATION (BY PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus."; Nature 313:450-458(1985).
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                                                                                                                                                             Score 1130; DB 1;
Pred. No. 9.3e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA.
                                                                                                                                                                                     Mismatches
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MEDLINE-85111157; PubMed-2982104;
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                                                                                                                             23342 MW;
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HIV; KO2013; NEF$BRU.
HIV; M19921; NEF$NL43
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P03405;
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Best Local S:
Matches 206
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Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.; "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTV) type IIIB).";
AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QEEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTGGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY
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-: FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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MEDILNE-97337445; PubMed-9194185;
GZCSESIEK S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,
Tjandra N., Wingfled P.T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
Viruses, Retroid viruses, Retroviridae, Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 206;
                                                                                                                                                                                                                                                                        MYRISTATE.
EDE64281A17C6735 CRC64;
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ID NEF_HVILW

AC 07052;

15-001-1998 (Rel. 36, Created)

DT 15-001-1998 (Rel. 36, Last sequence update)

DT 16-0CT-2001 (Rel. 40, Last annotation update)

DE Negative factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 1114; DB 1; 97.6%; Pred. No. 2.3e-90;
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EMBL; X01762; -; NOT_ANNOTATED_CDS.
PIR; A04007; ASLJVL.
HSSP; P03406; 1EFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                    HIV; K02083; NEFSPV22.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP binding.
LIPID MY
                                                                                                                                                                                                                                                                                                       206 AA; 23352 MW;
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Matches 201; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                      121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                  61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                            Gaps
                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=86177573; PubMed=3008154;
Arya S.K., Gallo R.C.;
"Thee novel genes of human T-lymphotropic virus type III: immune reactivity of their products with sera from acquired immune deficiency syndrome patients.";
                                                                                                                                                                                       1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: NEF HAS GYPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                            ö
                                                                                                                             Length 206;
                                                                                                                                                          1; Indels
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                              MYRISTATE.
; ED81F68F6B61278E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987 (Rel. 04, Created)
13-MGG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
                                                                                                                            Score 1111; DB 1;
Pred. No. 4.3e-90;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION,
PDB; 2NEF; 07-JUL-97.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding; 3D-structure.
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HIV; M11840; NEF$PCV12.
InterPro; IPR001558; F-protein.
                                                                              206 AA; 23414 MW;
                                                                                                                          Query Match 65.8%;
Best Local Similarity 97.1%;
Matches 200; Conservative
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Nature 330:266-269(1987).
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PO4324:
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Guy B., Kleny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                           FPDWQNYTPGPGIRYPLTFGWCYKLVPVEPEKLEEANKGENTSLLHPVSLHGMDDPEREV 180
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Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo Hong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1985).
                                                                                                                 Length 206;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                     MYRISTATE.
218F5B2980F79A46 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                 Score 1108; DB 1;
Pred. No. 7.8e-90;
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HSSP; P03406; 1EFN.
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
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                                                       206 AA; 23366 MW;
Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                 65.6%;
97.1%;
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Nature 330:266-269(1987).
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                                                                                                               Query Match
Best Local Simi.
Matches 200;
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P05855;
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Matches 185;
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ID NEF_HV1S3
AC P19545;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                             61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHPLKEKGGLEGLIHSQRRQDILDLMIHHTQGY 120
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Dandekar S.;
"Biological and molecular characterization of human immunodeficiency
virus (HIV-1BR) from the brain of a patient with progressive
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                        1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                                                                                                                               MEDLINE-89085613; PubMed-2789516;
Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I-FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITES, IT SEEMS TO DOWN PEGULATE THE CD4 (T4) ANTIGEN.
-I-MISCELLANBOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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                                                                                                                                      64.5%; Score 1088.5; DB 1; Length 205; 96.6%; Pred. No. 3.9e-88; 1.ve 3; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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218 AA; 25032 MW; FC4DAEA1045C460E CRC64;
                                     MYRISTATE.
8EC12F6650DDD111 CRC64;
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16-0CT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEWRFDSRLAFHHVARELHPEYFKNC 206
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01-0CT-1989 (Rel. 12, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                 205 AA; 23305 MW;
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LIPID 2
AIDS; Myristate; GTP-binding.
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M21098; AAA44222.1; -.
                                                                                                                                                                 Best Local Similarity 96.6
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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HIV; M21098; NEF$BRVA.
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P12479;
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NEF_HV1BN
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Length 218;

Score 1019; DB 1; Pred. No. 5e-82;

60.4%; 84.1%;

Query Match Best Local Similarity

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                                                                                                                                                                                                             ODILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLH 166
                                                                                                                                                                                                                                                                                                                              61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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                                                                                                                                                                           NTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRR 106
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      Gaps
                                                          1 MGGKWSKSSVVGWPTVRERMR------RAEPAADGVGAASRDLEKHGAITSS 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the viral genome.";
J. Virol. 64:4016-4020(1990).
-i. FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING AND ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINEd-2370688; MEDILINE-90317906; PubMed-2370688; MEDILINE-90317906; Cheng-Mayer C., Bauer D., Levy J.A., Dina D.; York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.; "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retrold viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                           59.6%; Score 1005.5; DB
86.4%; Pred. No. 7e-81;
tive 19; Mismatches
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   Mismatches
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   12;
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Best Local Similarity 86.44
Matches 178; Conservative
      Conservative
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RESULT 8 NEF\_HV1OY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montagnier L., Lecocq J.-P.; "HIV {\rm F/3}^{\prime} orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                             MEDLINE-85090453; PubMed-2578227; Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S., Stemplen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A.; Levy J.A., Dina D., Luciw P.A.; "Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                     POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; PubMed-3118220;
GUY B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an oncogene product.";
Nature 330:266-269(1987).
-i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                            Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11685;
                                                                21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
    210 AA
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EKEVLVWRFDSKLAFHHMARELHPEYYKDC
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                                              (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                Science 227:484-492(1985).
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Best Local Similarity 85.29
Matches 179; Conservative
  STANDARD;
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HSSP; P03406; 1EFN.
HIV; K02007; NEF$SF2.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                         21-JUL-1986 (
21-JUL-1986 (
16-OCT-2001 (
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NEF_HV1RH
ID NEF_HV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGGKWSKSSVVGWPTVRERMRRA----EPAADGVGAASRDLEKHGAITSSNTAATNAAC
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-1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DONN-REGULATE THE CD4(T4) ANTIGEN.
-1- MISCELLANEOUS: THE OXI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.1%; Score 997.5; DB 1; Length 211; 82.9%; Pred. No. 3.6e-80; tive 22; Mismatches 9; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11699;
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                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                      211 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 LVWKFDSHLAFRHMARELHPEYYKDC 205
                                                                LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AA; 24067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PF00469; F-protein; 1. ; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M26727; AAA83398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 82.9
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; M26727; NEF$OYI.
                                                                                                                                                                                                                   NEF_HV10Y
P20886;
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SEQUENCE
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                                                                                                                                                                                                                                                                       57 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 116
                                                                                                                                                                                                                                                                                                                                                                TQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 176
                                                                                                                                  Gaps
                                                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 56
                                                                                                                                                                                                      4
                                                                                    59.1%; Score 997; DB 1; Length 210;
85.2%; Pred. No. 4e-80;
11ve 16; Mismatches 11; Indels
MYRISTATE.
ED255233F8A17DAB CRC64;
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61 116 121 176 181

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                 Submitted (XXX-1987) to the HIV data bank.
-I- FUNCTION: NEF HAS GPPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 Q--EEEEVGFPVTPQVPLRPMTYRAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93021387; PubMed-1404605;
L1 Y., Hul H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                   Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                     Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.9%; Score 994; DB 1; Length 208; 84.6%; Pred. No. 7.3e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
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8F836FE8980F084C CRC64;
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                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23532 MW;
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HSSP; P03406; 1EFN.
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Best Local Similarity 84.61
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; M17451; NEF$RF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AA;
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                                                                                                                                                                           NCBI_TaxID=11701;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P35959;
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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGGKWSKSSVVGWPTVR-------ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA 50
         Koyanagi S., Chen I.S.Y.;
Subaitted (DEC-1988) to the HIV data bank.
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, II SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
and biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 991.5; DB 1; Length 214;
; Pred. No. 1.2e-79;
12; Mismatches 11; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRISTATE (BY SIMILARITY)
E188D43D7B084D04 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
   genome organization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 HGMDDPEREGLEWRFDSRLAFHHVARELHPEYYKN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M93258; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; 144001; 144001.
HSSP; P03406; 1EFN.
InterPro; 1PR001558; F-protein.
   'Complete nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA; 24532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00469; F-protein;
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Best Local Similarity 84.2
Matches 181; Conservative
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P20867;
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Gaps

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Indels

16;

us-09-509-239-13.rsp

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Best Local Similarity 84.2%
Matches 176; Conservative
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16-OCT-2001
                                                                                                                                                                                                                                                               NEF_HV1EL
P04604;
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                                                                                                                                                                                                                             51 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 110
                                                                                                                                                                                                                                        DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 170
                                                                                                                                                                                                                                                                                      Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.,
"Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4386(1990).
- PUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                        Gaps
                                                                                                                                                                                                     9
                                                                                                                                                                               1 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 50
                                                                                                                                                                                                     1 MGGKWSKHSVPGWSTVRERMRRAEPATDRVRQTEPAAVGVGAVSRDLEKHGAITSSNTAA
                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                               Length 216;
                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYRISTATE (BY SIMILARITY)
A0B1007D14E46E32 CRC64;
                                                                                MYRISTATE (BY SIMILARITY)
D163FFA8C71529DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                     181 HGMDDPEKEVLVWKFDSKLALHHVARELHPEYYKDC 216
                                                                                                                              58.1%; Score 981; DB 1, 81.9%; Pred. No. 1e-78;
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                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                         HGMDOPEREVLEWRFDSRLAFHHVARELHPEYFKNC
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Pfam; PF00469; F-protein; 1
                                HIV; M38429; NEF5JRCSF.
InterPro; IPROUSISSB; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
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                                                                                            216 AA; 24567 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M65024; AAA45073.1; -.
        EMBL; M38429; AAB03750.1;
HSSP; P03406; 1EFN.
                                                                                                                               Query Match
Best Local Similarity 81.99
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; M38428; NEF$SF162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11691;
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P19546;
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                                                                                             SEQUENCE
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Length 208;

DB 1;

57.7%; Score 974;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88039140; PubMed-3118220;
Guy B., Klany M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.,
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                  LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT 117
                                                                                                                                                                                                                                                                                                                       QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86245056; PubMed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African pattlents.";
                                                                                    MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 57
                                                                                                                                           1 MGGKWSK-RMSGWSAVRERMKRAEPAEPAADGVGAVSRDLEKHGAITSSNTAANNADCAW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an oncogene product.";
Nature 330.266-269(1987).
-!- FUNCTION: NEF HASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus..
NCBI_TaxID=11689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4CFF9F18AEAB503C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 927.5; DB 1; 79.1%; Pred. No. 4.7e-74;
4.1e-78;
ches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches
Pred. No. 4.1e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 REVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AA; 23612 MW;
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LIPID 2 2
SEQUENCE 206 AA; 23612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K03454; AAA44330.1; -. EMBL; A07108; CAA00617.1; -. HSSP; P03406; 1EFN. HIV; K03454; NEF$ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00469; F-protein;
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Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 46:63-74(1986).
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us-09-509-239-13.rsp

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AWLEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI 114
1 MGGKWSKSSVVGWPTVRERM-----RRAEPAADGVGAASRDLEKHGAITSSNTAATNAAC
             181
                                                   26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular characterization of human immunodeficiency virus from Laire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene."; Gene 52:71-82(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88039140; Pubmed-3118220; Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M., Guy B., Lecocq J.-P.; Montagnier L., Lecocq J.-P.; "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                  -!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
               1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                   QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG
                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11708;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87248097; PubMed-3036660;
Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
Sanchez-Pescador R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 54.0%; Score 911; DB 1; Length 212; Best Local Similarity 77.4%; Pred. No. 1.3e-72; Matches 164; Conservative 23; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC095A1B263047CF CRC64;
                                                                                                                                                                                                                                                                                                               Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYRISTATE
                                                                                                                                                                     180 VLEWRFDSRLAFHHVARELHPEYFKN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 AA; 24415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDS; Myristate; GTP-binding.
LIPID 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K03458; AAA45381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00469; F-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an oncogene product.";
Nature 330:266-269(1987).
                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; F26192; QQLJZR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P03406; IEFN.
HIV; K03458; NEF$Z6
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an oncogene
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P04602;
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THE PUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN.REGULATE THE CD4(T4) ANTIGEN.
ACTIVITIES, IT SEEMS TO DOWN.REGULATE THE CD4(T4) ANTIGEN.
ALDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
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                                 121 YNTQGIFPDWQNYTPGPGIRYPLIFGWCFELVPVDPREVEBATGGETNCLHPVCQHGME 180
YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90034200; PubMed-2806917; Spire B., Stre J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.; "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (NDK isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYRISTATE (BY SIMILARITY)
09036C2F81D45D5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                             207 AA
                                                                                                                                                                  | |||||:|||:|||:||| | |||:|||::|:|
| DIEREVLKWRFNSRLAFEHKAREMHPEFYKDC 212
                                                                                                                                DPEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human immunodeficiency virus.";
Gene 81:275-284(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA; 23748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M27323; AAA44874.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JQ0068; QQLJND.
HSSP; P03406; 1EFN.
HIV; M27323; NEF$NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                      NEF_HV1ND
P18801;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89228766; PubMed-2713163;
Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGGKWSKSSVVGWPTVRERMRRAEP---AADGVGAASRDLEKHGAITSSNTAATNAACAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 LEAQEEEEVGFPVKPQVPLRPMTYKAALDLSHFLKEKGGLDGLIYSQKRQDILDLMVYHT
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88219542; PubMed-3369091;
MEDLINE-88219542; PubMed-3369091;
MEDLINE-88219542; Outlier, Franchini G., Aldovini A., Collaiti E.,
Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
"Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
--- FUNCTION: NEF HAS GTPAS, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN.
--- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 QGYFPDWQNYTPGPGIRYPLTFGWCFKLVPVEPEKIEEANKGENNCLLHPMSQHG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 842; DB 1; Length 182;
; Pred. No. 1.2e-66;
11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (Zaire H2321 isolate)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                       Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                          01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annoration update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
182 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AA; 20632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.4%;
Matches 153; Conservative 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M17449; AAA44858.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; M17449; NEF$MN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATIENT IN 1984.
                                                                                                                                                                                                    NCBI_TaxID=11696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11692;
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P05859;
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SEQUENCE
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NEF_HV1ZH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPDWQNYTPGPGVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IFPDWQNYTPGPGIRYPLTFGWCFQLVPVDPQEVERATEREDNCLLHPMCQQGMEDPERQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  YFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic diversity from other HIV-1 isolates.";
AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
--i- FUNCTION: NEF HAS GIPAGE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-91090981; PubMed-2265025;
Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
Carawell J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.7%; Score 872; DB 1; Length 205; Best Local Similarity 75.1%; Pred. No. 3.3e-69; Matches 154; Conservative 24; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYRISTATE (BY SIMILARITY)
; 869AB03E6E7893C4 CRC64;
                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-GCT-2001 (Rel. 40, Last annotation update)
18-9ative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11703;
                                                                                                                                                                                                                                                   205 AA
                                                                                       180 VLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEWRFDSRLAFHHVARELHPEYFKN 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 AA; 23253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M62320; AAA75023.1; -. HSSP; P03406; 1EFN.
                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                NEF_HV1U4
P24741;
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RESULT 18

NEF\_HV1MN

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4; Gaps 57 us-09-509-239-13.rsp

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                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88039140; PubMed-3118220; Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M., Montagnier L., Lecocq J.-P.; "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                            58 LEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 116
                                                                                                                                                                                                                                                                                                                                                                                                                        TQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-86245056; Pubmed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
McCormick J., Ou C.Y., Myers G., Smith T., Chen E.; "Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence comparison to recent isolates and
                                                                                                                                                                                                                                                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 57
                         Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                     2 2 MYRISTATE (BY SIMILARITY).
205 AA; 23306 MW; EA55B18AF412A9D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                  49.6%; Score 837; DB 1;
llarity 73.2%; Pred. No. 3.8e-66;
Conservative 23; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 EREVIAWKFDSSLARKHLAREMHPEFYKD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 EREVLEWRFDSRLAFHHVARELHPEYFKN 205
                                                                                                                                                                                                                                InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                                                                                    EMBL; M15896; AAB53951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                       HIV; M15896; NEF$Z321.
                                                                                                                                                                                               B44963; B44963.
; P03406; 1EFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of two isolates from Cell 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11697;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simil
Matches 153; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEF_HV1MA
PO4603:
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
NEF_HV1MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Huet T., Cheynler R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990)
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVG----AASRDLEKHGAITSSNTAATNAAC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY
                                                         FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 834.5; DB 1; Length 209; Pred. No. 6.4e-66; 26; Mismatches 30; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D0B30A2442C8CC44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001558; F-protein, Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 AA; 23644 MW;
oncogene product.";
ture 330:266-269(1987).
- FUNCTION: NEF HAS GTPASE,
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X04415; CAA28017.1; -. EMBL; A07116; CAA00624.1; -. HSSP; P03406; IEFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.48;
70.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.1:
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; K03456; NEF$MAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-AUG-1990 (
16-OCT-2001 (
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P17664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                               1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
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0
                                                                                                                                                                                                                                             49.3%; Score 832; DB 1; Length 205; 70.2%; Pred. No. 1e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11702;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE (BY SIMILARITY).
704A17E54763A99B CRC64;
                                                                                                                                                               MYRISTATE (BY SIMILARITY).; 21E0A3EC99F1811F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA.
                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LVWRFDSRLALRHIAREQHPEYYKD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LEWRFDSRLAFHHVARELHPEYFKN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88219542; PubMed-3369091;
                                  PIR; S09991; ASLJIK.
HSSP. P03406; 1EFN.
HIV; X52154; NEFSCP2.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS, Myristate; GTP-binding.
2 2 MYSSEQUENCE 239 AA; 26799 MW;
                                                                                                                                                                                   205 AA; 23850 MW;
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                 X52154; CAA36408.1;
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.2'
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; M17450; NEF$SC
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P05857;
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                   EMBL;
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MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Rivier.
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
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-:- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 ADDS A STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
                                                                                                                                                                                                                                        QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                       61 QEEEEVGFPVRPQVPLRPWTYKAAVDLSHFLKEQGGLEGLI--TPREDKISLICGSTTHK 118
                                                                                                                                                                                                                                                                                                                                                                                      119 ATSLIGRTTHGGGGSDIPLCFGWCFKLVPVKPEKIEEANEGENNSLLHPMSLHGMEDPER 178
                                                                                                                                                                          9
                                                                                                                  MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                    121 FPDWQNYT - - PGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87299196; PubMed-3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.; "Complete nucleotide sequences of functional clones of the AIDS
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11706;
Length 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou Gallo R.C., Wong-Staal F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
; DB 1;
1.7e-64;
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                                                       16; Mismatches
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   Score 819;
Pred. No. 1
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P04601; 009780;
I3-AUG-1987 (Rel. 05, Created)
15-JUL-1999 (Rel. 38, Last sequ
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K03455; AAB50263.1; -.
EMBL; AF033819; AAC82597.1; -
HSSP; Q70627; 2NEF.
   48.5%;
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Nature 330:266-269(1987).
                                                             Conservative
                                  Similarity
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                                                             Matches 157;
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   Query Match
Best Local S
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HIV; M15654; NEF\$BH102.

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Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULARE THE CD4(T4) ANTIGEN.
-i- MISCELLANEOUS: IN THIS ISOLATE A WUTATION IN POSITION 124 ADDS A STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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MEDLINE-85111123; Pubmed-2578615;
Rathor L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.K., Rafalski J.A., Whitehorn E.A.,
Baumelster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
                                                                                                                                                                                                                                                           Length 123;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                        PHOSPHORYLATION (BY PKC).
B5007753CCD244CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
13-MG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                       18.2%; Score 645; DB 1;
1larity 98.4%; Pred. No. 1.2e-49;
Conservative 1; Mismatches 1
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POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
   123 AA.
                                                                                                                                                                    123 AA; 13692 MW;
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Nature 330:266-269(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                          Best Local Similarity
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13-AUG-1987 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                     Matches 121;
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P03404;
                                                                                                                                           MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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NEF_HV1B1

NEF_HV1B1

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EMBL; M15654; AAA44206.1; -.

PIR; A04005; ASLJH3 HSSP; Q70627; 2NEF.

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MEDLINE=85228248; PubMed=2988795;
MEDLINE=85228248; PubMed=2988795;
MEDLINE=85228248; PubMed=2988795;
Shaw G.M., Wong-Staal F., Reddy E.P.;
"HTLV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";
cell 41:979-986[1985].
THANS-41979-986[1985].
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                          61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTYGY 120
                                                                                                                                                                                                                                                                                                       61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                 Gaps
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STRAIN=ISOLATE BH10;
MEDLINE=85111123; Bubmed=2578615;
Match L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
                                                                                                                                                                                                                                              1 MGGKWSKSSVVGWPTVRERMRAEPAADGVGAASRDLEKHGAİTSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-!- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.
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Nature 313:277-284(1985).
                                                                                                                                         Length 123;
                                                                                                                                                                                 3; Indels
                                                           MYRISTATE.
0811735345F0EB8B CRC64;
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                                                                                                                                       Score 638; DB 1;
Pred. No. 5.1e-49;
0; Mismatches 3.
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(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
LIPID 2 2 MYR
                                                                                123 AA; 13606 MW;
                                                                                                                                         Query Match 37.8%;
Best Local Similarity 97.6%;
Matches 120; Conservative
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13-AUG-1987 (
16-OCT-2001 (
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P04606;
                                                                                SEQUENCE
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us-09-509-239-13.rsp

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Nature 313:450-458(1985).
--- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 61
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Musbirne-55111157; Pubmed-2982104;
Mussing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
Capon D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ranscription regulation; Activator; RNA-binding; Nuclear protein;
                      EMBL; M14100; AAA44676.1; -.
EMBL, M15654; AAA4199.1; -.
HIV; M15654; TAT$HIV0.
HIV; M14100; TAT$HIV0.
InterPro; IPR001831; HIV_Tat.
PRIM: PRO00539; TAT; 1.
PRIMIS; PR00055; HIVTDOMAIN.
Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   numan immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.8%; Score 486; DB 1; Length 86 Best Local Similarity 100.0%; Pred. No. 6.4e-36; Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  4DD609415FAF9015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4DD5C6415FAF9015 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAT protein (Transactivating regulatory protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQTHQVSLSKQPTSQSRGDPTGPKE 86
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(Rel. 05, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001831; HIV_Tat.
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                                                                                                                                                                                                                                                                                                                                                  9784 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; K02083; TAT$PV22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 05, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00539; Tat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAT_HV1PV
P04607;
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                                                                    EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                   Gaps
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (clone 12) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4DD609414FBE9115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    TAT protein (Transactivating regulatory protein).
Pred. No. 1.7e-35;
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Pred. No. 3.2e-35;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                           04, Created)
05, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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PIR; AO4017; TNLJ12.
HIV; M11840; TAT$FCV12.
InterPro; IPR01831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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ilarity 98.8%;
Conservative
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             Best Local Similarity 98.8
Matches 84; Conservative
                                                                                                                                                                                                                                                                            STANDARD;
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nes 84; Conserv
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                                                                                                                                                                                                                                                                                                               (Rel.
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                                                                                                                                                                                                                                                                                                             20-MAR-1987
13-AUG-1987
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                                                                                                                                                                                                                                                                        TAT_HV112
P04326;
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                                                                                                                                                                                                                                       RESULT 27
TAT_HV112
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Matches
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TAT\_HV1BR

Length 86;

DB 1;

Score 481;

28.5%;

Query Match

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TAT_HV1H2
P04608; 009778;
13-AUG-1987 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999
16-OCT-2001
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                                                                                                                                                                                                                                                                                   SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                   SEQUENCE FROM N.A. (CLONE PNL4-3).

Buckler C.E., Buckler white A.J., Willey R.L., McCoy J.;

Buckler C.T., Buckler white A.J., Willey R.L., McCoy J.;

Submitted (Jun-1988) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATIOR RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> N (IN CLONE PNL4-3).

T -> M (IN CLONE PNL4-3).

PPOG -> AHON (IN CLONE PNL4-3).

V -> A (IN CLONE PNL4-3).

P -> S (IN CLONE PNL4-3).

9B1B4A915FAF8A14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 470; DB 1; Length 86;
Pred. No. 1.6e-34;
0; Mismatches 3; Indels
                                                                                 Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
                                                                                                                                                      Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.; "Nucleotide sequence of the AIDS virus, LAV.";
                                                                                      Viruses; Retroid viruses; Retroviridae; Lentivirus.
                            13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
 86 AA.
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  PRT;
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                                                                                                                                          MEDLINE-85099333; PubMed-2981635;
                        (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001831; HIV_Tat.
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Best Local Similarity 96.5%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9769 MW;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; KO2013; TAT$BRU.
HIV; M19921; TAT$NL43.
                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00539;
                       .3-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAT_HV1RH
P05908;
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VARIANT
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TAT_HVIRH
ID TAT_F
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DT 01-
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                                                                                                                                                                                                                                                                                                                                                                                           Cell 45:637-648(1986).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION ANN/OR ELONGATION FROM THE LIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         franscription regulation; Activator; RNA-binding; Nuclear protein;
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MEDILIDE-81299196; Pubmed-3040055;
Rather L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
                                                                                                                                                                          MEDLINE-86218077; PubMed-2423250; Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal B.C., Mong-Staal B.C., In the envelope gene of HTLV-III/LAV, the retrovirus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete nucleotide sequences of functional clones of the AIDS
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numun numunodeficiency virus type l (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11706;
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91.9%; Pred. No. 1.2e-33;
live 3; Mismatches 4;
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-:- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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Last annotation update)
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AIDS Res. Hum. Retroviruses 3:57-69(1987).
[2]
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InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1
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Best Local Similarity 91.99
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                                                                                                                                                                      SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
               Rather L., Fisher A., Jagodzinski L.L., Mitsuya'H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATIOR RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; RNA-binding; Nuclear protein;
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Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K03455; AAB50256.1; -. EMBL; AF033819; AAC82591.1; HIV; K03455; TAT$HXB2.
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Query Match 26.9%; Score 454; DB 1; Length 86;
Best Local Similarity 94.1%; Pred. No. 4e-33;
Matches 80; Conservative 0; Mismatches 5; Indels 0; Gaps
Qy 209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPGG 268
Db 2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPGN 61

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QY 269 SQTHQVSLSKQPTSQSRGDPTGPKE 293

62 SQTHQASLSKQPTSQPRGDPTGPKE 86

Search completed: August 26, 2002, 08:15:41 Job time: 345 sec

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			12, C 12, L 19, L	/irus 3; Ret	Z., Pac Sonne a clini study." the EM GTPASE S TO DOI 3.1;	1) 1. State. 28 MW; .9%; .5%;	RMRRAE             RMRRAE 4TYKAA
663.9 67.3		PRELIMINARY,	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.	odeficiency v troid viruses 11676;	DM N.A.  In 10 , Yun  Alni U , Yun  Thatlons an  pidemiology i  UON-1997) to  UON-1997) to  ES, IT SEEM  180; AAD0145i  5, IEFN  PRO0158; F:	69; F-proteil inding; Myrii 206 AA; 2333 106 AB; 2333 200 AB; 233	KSSVGWPTVREI 
117 118 119 119 110 110 110 110 110 110 110 110		ULT 1 M24 Q9WM24	01-NOV-1999 01-NOV-1999 01-DEC-2001 NEGATIVE FAC	Human immunc Viruses; Rei NCBI_TaxID=1	RN [1] RP SEQUENCE FROM N.A. RC STRAIN-12-IT; RA Visco Comandini (1, Yun 2., I R Johansson B., Vahlne A., Soni RT HIV-1 nef mutations and cluin RT molecular epidemiology study RL Submitted (JUN-1997) to the I CC -1- SIMILARITY: NEF HAS GIPAA. CC ACTIVITIES, IT SEEMS TO I DR EMBL; AF011480; AAD01458.1; DR HSSP; P03406; 1EFN DR INTERPRO; IPRO01558; F-PFOTCE.	Pfam; PF004 AIDS; GTP-b SEQUENCE : uery Match est Local Sim atches 205;	1 MGGKWSI       1 MGGKWSI 61 QEEEEV
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   Viruses; Retroid
NCBI_TaxID=11676;
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Johansson B., Vahlne A., Sonnerborg A.;
"HIV-1 nef mutations and clinical long-term non progression: a
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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99.0%; Pred. No. 2.5e-94;
tive 1; Mismatches 1;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence upd
01-DEC-2001 (TrEMBLrel. 19, Last annotation u
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23341 MW;
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
01-DEC-2001 (TrEMBLrel, 19,
NEGATIVE FACTOR (F-PROTEIN)
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Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K., Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.; Recovery of virtually full-length HIV-1 provirus of diverse subtypes from primary virus cultures using the polymerase chain reaction."; Virology 213:80-86(1995).
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MUL 1016942; 284-291(1986).

EMBL: U26942; AAB60579.1; --

SEQUENCE 206 AA. 23367 MW; 65AF3B6184DC2FE7 CRC64;
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                                                                                                                                                                                                       Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4 (T4) ANTIGEN.
HSSP, P03406; 1EFN.
InterPro; IPR001558; F-protein.
Pfam, PF00469; F-protein.
SEQUENCE 206 AA; 23428 MW; 9F94AEB9CAFDC6F6 CRC64;
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                                                                                                                                Fang G., Welser B., Visosky A., Burger H.; "Constructing full-length chimeric HIV-1 molecular clones by PCR-
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
Retroid viruses; Retroviridae; Lentivirus
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MEDLINE=86281827; Pubmed=3016298;
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MEDLINE=96036482; PubMed=7483282;
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01-DEC-2001 (TrEMBLrel.
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AIDS 6:1427-1436(1992).
-!- SIMILARITY: NEF HAS GTRASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- SILIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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llarity 97.1%; Pred. No. 7e-93;
Conservative 3; Mismatches 3;
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Score 1115; DB 15
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
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"HIV-1 nef mutations and clinical long-term non progression: a molecular epidemiology study.";

Submitted (JUN-1997) to the EMBL/GenBank/DBB databases.

-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(f4) ANTIGEN.
                                                                                                                                                                                                                                     Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A., Johansson B., Vahlne A., Sonnerborg A.; "HIV-1 nef mutations and clinical long-term non progression: a
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.3e-92;
2; Mismatches 4;
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-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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Pfam: PF00469; F-protein: 1.
AIDS: GTP-binding; Myristate.
SEQUENCE 206 AA; 23439 MW; 8478CF194D39D5B9 CRC64;
                                                                                                         OED69927C2E03BB6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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4; Mismatches 4;
                                                                                                                                                                       Score 1104; DB 15;
Pred. No. 1.6e-92;
1; Mismatches 5;
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Best Local Similarity 96.1%; Pred. No. 3e-
Matches 198; Conservative 4; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93152025; PubMed-1301062;
EMBL; AF011469; AAD01447.1; -. HSSP; P03406; 1EFN. InterPro; IPR001558; F-protein.
                                                           Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23345 MW;
                                                                                                                                                                       Query Match 65.4%;
Best Local Similarity 97.1%;
Matches 200; Conservative
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Q9PXW8;
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-95074930; PubMed=7983770;
Fang H., Pincus S.H.;
Fang H., Pincus S.H.;
"Unique insertion sequence and pattern of CD4 expression in variants selected with immunotoxins from human immunodeficiency virus type 1-infected T cells.";
J. Virol. 69:75-81(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotoxin-resistant variant T cell line.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF070521; AAC28453.1;
HSSP; P03406; 1EFN.
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Fang H., Pincus S.H.;
"Spontaneous activation of human immunodeficiency virus type 1 in
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Pfam: PF00469; F-protein; 1.
Aldbs: GTP-binding; Myristate.
SEQUENCE 206 AA; 23334 MW; 3E2B9C4017FDCA68 CRC64;
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(27 KDA PROTEIN).
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                              206 AA
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PRT;
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Q85588:
01-NOV-1996 (TrEMBLrel: 01, C
01-NOV-1996 (TrEMBLrel: 01, L;
01-DEC-2001 (TrEMBLrel: 19, L;
NEGATIVE FACTOR (F-PROTEIN) (:
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Matches 197;
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M.L., Haseltine W.A., Arya S.K.,
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                                                                                                                                                                                                                              virus type III.";
Nucleic Acids Res. 13:8219-8229(1985).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, II SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                "Polymorphism of the 3' open reading frame of the virus associated with the acquired immune deficiency syndrome, human I-lymphotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
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MEDLINE-89352106, PubMed-2765297;

Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo
Macchi B., Manglano N., Verani P., Rossi G.;

"Biological and molecular characterization of producer and non
producer clones from HUT-78 infected with a patient HIV isolate."
AIDS Res. Hum. Retroviruses 5:385-396(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 8.6e-92;
4; Mismatches 3;
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Viruses; Retroid viruses; Retroviridae.
NCBI_TaxID=11966;
                                                                                          MEDLINE-86067228; PubMed-2999715;
Ratner L., Starcich B., Josephs S.F.,
Livak K.J., Petteway S.R.Jr., Pearson
Wong-staal F.;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23419 MW;
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96.6%;
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF047084; AAD02458.1; -. HSSP; P03406; 1EFN.
                                                                                         Int. J. Immunopharmacol. 3:17-23(1990).
--- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL: 211530; CAA77629.1;
HSSP: P03406; IEFN.
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                                        an infected but
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                                                                                                                                                                                                                                                                                                                                                                            Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                             InterPro: IPR001558; F-protein.
Pfam: PF00469; F-protein: 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23398 MW; A31CC7244BBB2B43 CRC64;
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Last sequence update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                       Score 1096; DB 15;
Pred. No. 8.6e-92;
3; Mismatches 4;
Borsetti A., Saggio I., Verani P., Rossi G.;
"Variability of HIV-1 virus: characteristics of
productive clone.";
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                                                                                      . Immunopharmacol. 3:17-23(1990)
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Pram: PR00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23512 WW; 1
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Best Local Similarity 96.6%;
Matches 199; Conservative
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97; Conservative
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SEQUENCE FROM
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Q74913
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VIROLOGY 233:245-250(1996)

ACTIVITIES, IT SERMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN. EMBL; U44443; AAB38195:1;

HSSP: Q70627; ZNEF.
         61 QEEEEVGFPVRPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIYSQRRQDILDLWIYHTGGY 120
                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                   121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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0
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Last annotation update)
(27 KDA PROTEIN)
                                                                                                                                                                   Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 1090; DB 15;
Pred. No. 3e-91;
6; Mismatches 4;
                                                                                                                                          206 AA.
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                                                                                   181 LEWRFDSRLAFHHVARELHPEYYKNC 206
                                                                                                                                                            Created
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23617 MW;
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Best Local Similarity 95.1%;
Matches 196; Conservative
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Q89561
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61
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Q74905
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MEDLINE-96400183; PubMed-8806559;
Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A., Hahn B., Powderly W., Arens M.;
"Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects at different stages of disease.";
Virology 223:245-250(1996).
-: SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL. U44453; AABS 205.1;
-- HSSP: P03406; IEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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                                                                                                                           Arens M.O., Ratner L., Joseph T., Bandres J.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(F4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1087; DB 15; Length 206; Pred. No. 5.7e-91;
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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llarity 95.6%; Pred. No. 8.6e-91;
Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 A.A.
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                                                                                                                                                                                                                     EMBL; U44448; AAB382001; --
EMBL; U44447; AAB38199.1; --
HSSP; Q70647; ZNEF.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23629 MW; BF
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23649 MW; 1
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01-DEC-2001 (TrEMBLrel. 19,
NEGATIVE FACTOR (F-PROTEIN)
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01-NOV-1996 (TrEMBLrel 01,
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Matches 195; Conservative
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Best Local Similarity
Matches 196; Conserv
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RESULT Q74917

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MEDLINE—96400183; PubMed—8806559;
MEDLINE—96400183; PubMed—8806559;
MEDLINE—96400183; PubMed—8806559;
METAIL I., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,
METAIL I., Powderly W., Arens M.;
METAIL I., Powderly W., Arens M.;
METAIL I., Powderly W., Arens M.;
METAIL I., Powderly W., Arens M.;
METAIL I., Powderly W., Arens M.;
METAIL I., METAIL I., SERMS TO BOWN-REGULATE THE CD4(T4) ANTIGEN.
METAIL: U44444; AAB38206.1;
METAPRO, IPRO01558; F-protein.
METAPRO, IPRO01558; F-protein.
METAPRO, PEDLAGIN; MYTISTATE.
METAPRO, METAPRO, METAIL I.
METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, METAPRO, META
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-! - SIMILARITY: NEF HAS GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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Last sequence update)
Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 3e-90;
5; Mismatches 5;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
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ilarity 95.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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01-DEC-2001
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Q74915;
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-I. SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.

HSSP; P03406; IEEN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Q74914;
01-NOV-1996 (TrEMBLrel. 01,
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ID Q74914
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MEDLINE-96400183; PubMed-8806559;
Rather L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A., Hahn B., Powderly W., Arens M.;
"Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects at different stages of disease.";
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                                                                                                       Gaps
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-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.
HSSP; Q70627; ZNEF.
INTERPOOL IPROU1558; F-protein.
Fam: PF00469; F-protein.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23488 MW; F0596D6FAAA81A05 CRC64;
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                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
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                                                             Length 206;
                                                                                                     Indels
ESBD6FA0B70FC175 CRC64;
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Last annotation update)
(27 KDA PROTEIN)
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                                                         Score 1079; DB 15;
Pred. No. 3e-90;
5; Mismatches 4;
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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23648 MW;
                                                         Query Match 63.9%;
Best Local Similarity 95.6%;
Matches 195; Conservative
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Best Local Similarity
Matches 194; Conserv
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206
SEQUENCE
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pVUBB expression system based on the major lipoprotein (Opri) from the outer membrane of Pseudomonas aeruginosa.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL, AF166101; AAD47831.1;
-- RAF66101; AAD47831.1;
-- INTERPROSSING IERN.
INTERPROSSING IERN.
INTERPROSSING IERN.
ANDERS: GTP-binding; Myristate.
NON_TER
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"HIV-1 Strains from a cohort of American subjects reveal the presence
of a V2 region extension unique to slow progressors and non-
progressors.";
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                                                                                                                                                                                                                                                                                                                                              Canas-Ferreira W.F.; "Cloning and expression of HIV-1 nef gene in the carrier-adjuvant
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                                                                                                                                                                                                                                                                                             STRAIN-HIV-1LAI;
Piedade J., Esteves A., Parreira R., Venenno T., Barros M.F.,
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Pred. No. 5.5e-90;
0; Mismatches 5; Indels
                                                                Last sequence update)
Last annotation update)
(27 KDA PROTEIN) (FRÄGMENT).
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Last sequence update)
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Best Local.Similarity 97.5%;
Matches 197; Conservative
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                                                                                                                       NEGATIVE FACTOR (F-PROTEIN)
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PRELIMINARY;
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Q9W7X3;
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ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP, P03406, 1EFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        progressors.";
AIDS 0:0-0(2000).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF203198; AAF25320.1; -.
HSSP; P03406; 1EFN.
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                                                                                          081DF3A12E5A7576 CRC64;
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Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.3e-89;
5; Mismatches 8;
                                                                                                                         Score 1072; DB 15;
Pred. No. 1.3e-89;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23420 WW; 1
                                                         nterPro; IPR001558; F-protein.
                                                                Pfam: PF00469; F-protein: 1.
AIDS: GTP-binding: Myristate.
SEOUENCE 206 AA; 23510 MW;
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93.7%;
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Best Local Similarity 94.7%;
Matches 195; Conservative
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Matches 193; Conservative
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Q9Q595;
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GYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER 178
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.
EMBL; AF011470; AAD01448.1;
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FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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Last annotation update)
(27 KDA PROTEIN).
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus;
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Pred. No. 1.6e-89;
3; Mismatches 7;
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; I.
AIDS; GTP-binding; Myristate.
SEQUENCE 208 AA; 23681 WW;
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illarity 94.2%;
Conservative
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Best Local Similarity
Matches 196; Conserv
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Query Match
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Q9W7U0
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AIDS Res. thum. Retroviruses 16:1855-1868(2000).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(74) ANTIGEN.
                                                                                                                                                                                                                     J. Neurovirol. 4:0-0(1998).
-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP: P03406; 1EFN.
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"Functional and structural defects in HIV-1 nef genes derived from
                                                                                         Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of F
I positive individuals/AIDS patients with or without AIDS dementia
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                                                              McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 206;
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SEQUENCE 206 AA; 23499 MW; DEE21CAF05891D6B CRC64;
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Last annotation update)
(27 KDA PROTEIN)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 5.7e-89;
9; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.3%; Score 1068; DB 15;
91.7%; Pred. No. 3e-89;
live 14; Mismatches 3;
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MEDLINE-21002575; PubMed-11118071;
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                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR001558; F-protein.
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23464 MW;
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Matches 189; Conservative
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SEQUENCE FROM N.A.
STRAIN-PATIENT 27;
MCPhee D.A., Greenway A.L., Holloway G., Smith K!, Deacon N.,
Pemberton L., Brew B.J.;
Anomalies in Nef expression within the central nervous system of HIV-
1 positive individuals/AIDS patients with or without AIDS dementia
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                                                                                      QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYL.

ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF064675; AC18375.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
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Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Local Similarity 91.7%; Pred. No. 7e-89;
les 189; Conservative 13; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                              206 AA.
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Pfam; PF00469; F-protein; I.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23514 MW; I.
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Best Local Similarity Matches 192; Conserv

Query Match

Length 206;

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Length 206;

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FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang B., Saksena N.K.;
"HIV-1 Strains from a cohort of American subjects reveal
of a V2 region extension unique to slow progressors and n
                                                                                                              2255A447ECE85456 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                  62.9%; Score 1061; DB 15;
91.7%; Pred. No. 1.3e-88;
ive 12; Mismatches 5;
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HSSP. P03406; 1EFN.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23472 MW; 22
                                                                                                                                                                                       Best Local Similarity 91.79
Matches 189; Conservative
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Matches 191; Conserv
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-! SIMILARIY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING EMBL; AF063922; AAC17933.1; -...
HSSP: P03465; IEEN.
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-!- SIMILARITY: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-PATIENT 27;
MCPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemborton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of F
I positive individuals/AIDS patients with or without AIDS dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4D5AEDF55FAE93E3 CRC64;
                                                    01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                numman immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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 206 AA
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23348 MW; 4
                              01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19,
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PRELIMINARY;
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STRAIN-PATIENT 27;
McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of HIV-
1 positive individuals/AIDS patients with or without AIDS dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FPDWQNYTPGPGIRYPLTFGWCYKLVPVEQEKVKKANEGKNTSLLHPMSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                                                    J. Neurovirol. 4:0-0(1998).
-i- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEBMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
BEBL; AF064677; AAC18378.1;
HSSP; P03406; IEFN.
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23442 MW; DC6A96AF05891D6B CRC64;
                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
                                                                                                                                                                                                                         Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11676;
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                         LEWRFDSRLAFHHVARELHPEYFKNC 206
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

Amino acid sequence of a His tagged LipD-Nef-Tat linked protein. HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load. Location/Qualifiers 1.109 /note= "ProtD fusion partner" (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. AAG63235 standard; Protein; 411 AA Human immunodeficiency virus. 2000GB-0002200. 2000GB-0009336. 2000GB-0013806. 29-JAN-2001; 2001WO-EP00944 2000WO-EP05998 (first entry) WO200154719-A2 14-APR-2000; 06-JUN-2000; 28-JUN-2000; 31-JAN-2000; 01-OCT-2001 02-AUG-2001 Synthetic AAG63235; Peptide Voss G; AAG63235 

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HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral
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                                                                                              The present sequence represents a His-tagged Nef-Tat linked protein of HIV, with a lipidation signal sequence (LipoD) which is removed after processing and a ProtD fusion partner. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV 9p120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with 9p120 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of Colf+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat
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                              New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                 1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL
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                                                                           Disclosure; Fig 1; 90pp; English
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WPI; 2001-476172/51.
N-PSDB; AAH42879.
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The present sequence represents a fusion protein comprising LipoD-HIV-1 Tat. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sshssnmantqmksdkillahrgasgylpehtleskalafaqqadyleqdlamtkdgrlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTGGYFPDWQNYTPGPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                   HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2246; DB 20;
Pred. No. 1.3e-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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99.6%; Score 2246; D
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 410; Conservative 0; Mismatches
                                                                                                                                                                          SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                  WPI; 1999-302282/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 AA;
                                                                                                                                                                                                                                                                                         N-PSDB; AAX35691
W09916884-A1
                                                                                      17-SEP-1998;
                                                                                                                                26-SEP-1997;
                                         08-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                      Bruck C,
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61 VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTGGYFPDWQNYTPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 410; Conserv
                                                                                                                      AAY02353;
                                                                                           AAY02353
                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                    Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                      or Nef
gp120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEÌQSLEMTENFETMGGKWSKSSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                    New use of a human immunodeficiency virus (HIV) Tat, or Nef, linked to Tat (Nef-Tat) protein or polynucleotide and an HIV protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%; Score 2246; DB 22;
100.0%; Pred. No. 1.3e-204;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                     Location/Qualifiers
1..111
/note= "ProtD fusion partner"
                                                                                                                                                                                                                                         SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 90pp; English
           Human immunodeficiency virus.
                                                                                                                                                                       31-JAN-2000, 2000GB-0002200.
14-APR-2000; 2000GB-0009336.
06-JUN-2000, 2000GB-0013B6.
28-JUN-2000, 2000GB-0013B98.
                                                                                                                                              2001WO-EP00944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 410; Conservative
                                                                                                                                                                                                                                                                                            WPI; 2001-476172/51.
N-PSDB; AAH42881.
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                                                                                           WO200154719-A2
                                                                                                                                              29-JAN-2001;
Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                    Peptide
                                                                                                                                                                                                                                                                    Voss G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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Gaps

Indels

Length 411;

20;

99.4%; Score 2242; DB 20 99.8%; Pred. No. 3e-204;

0; Mismatches

Conservative

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comprising LipoD-HIV-1
                                                                                                                                                                                                                                                                                                                                              gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a fusion protein comprising Lipo Tat.His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in vaccine to prevent HIV infection.
                                            413
                        SYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                       fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                         representative LipoD-Tat-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0020585
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godart SAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-302282/25
N-PSDB; AAX35689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 AA;
                                                                                                                                                                                                                                                                                                                                                 nef gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1998;
                                                                                                                                                                                                                                                           09-JUL-1999
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Sequence
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                                                                                                                          AAG63234;
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                                                                                                    AAG63234
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                                                                                                                                                                                                                                                                                                                             The present sequence represents a fusion protein comprising LipoD-HIV-1 Nef-His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Tat protein. The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVT 180
360
       HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein; vaccine; HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       HHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALG
                                                                                                                                                                                                                                                                                                                                                                                                 Length 324;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Score 1706.5; DB 20;
Pred. No. 1.6e-153;
; Mismatches 0; II
                                                                                                                                                                                                                                                                                                  partner
                                                                                                                           A representative LipoD-Nef-His fusion protein.
                                                                                                                                                                                                                                                                                                  or Nef protein linked to a fusion
                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLÒGICALS.
                                                                                                                                                                       Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 66pp; English.
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                                                                                AAY02352 standard; Protein; 324
                                                                                                                                                                                                                                                                                                                                                                                                 75.78;
78.88;
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                                                                                                                                                                                                                                 97GB-0020585
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                             Godart SAG,
                                                                                                                                                                                                                                                                           WPI; 1999-302282/25.
N-PSDB; AAX35688.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                            324 AA;
                                                                                                                                                                                                                   17-SEP-1998;
                                                                                                                                                                                                                                 26-SEP-1997;
                                                                                                                                                                                     WO9916884-A1
                                                                                                             09-JUL-1999
                                                                                                                                                                                                    08-APR-1999
                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                              AAY02352;
                                                                                                                                                                                                                                                             Bruck C,
                                                                                                                                                                                                                                                                                                 HIV Tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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The present sequence represents a His-tagged Nef protein of HIV, with a lipidation signal sequence (LipoD) which is removed after processing. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat. HIV Nef. or Nef-Tat: and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
                              241 gvrypltfgwcyklvpvepdkveeankgentsllhpvslhgmddperevlewrfdsrlaf 300
                                                                                                                        HHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALG 360
GVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of, a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
                                                                                                                                                                                                                                                                                         361 ISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKET$GHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a His tagged LipD-Nef of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ProtD fusion partner"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG63234 standard; Protein; 324
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2000GB-0009336.
2000GB-0013806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Human immunodeficiency virus.
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N-PSDB; AAH42878.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2000;
14-APR-2000;
06-JUN-2000;
28-JUN-2000;
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Length 324;

DB 22;

75.7%; Score 1706.5;

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WPI; 2001-476172/51.
N-PSDB; AAH42880.
                                 Best Local Similarity
Matches 323; Conser
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 326
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06-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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  Sequence
                          Query Match
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AAG63236
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                                                                                                                                                        300
                                                                                                                                                               HHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALG 360
                                                       VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVV 120
                                                                                                                                                                                                                                                                                                                                              : fusion protein; HIV nef gene; Nef protein; Tat protein; infection; protein D.
         Gaps
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                                 1. CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL
                                                                                       GWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVT
                                                                                                                                                        GVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAF
                                                                                                                      PQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGP
        87;
                                                                                                                                                                                                                        361 ISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 411
                                                                                                                                                                                                                                       -----tsghhhhh 324
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or Nef protein linked to a fusion partner
Pred. No. 1.6e-153;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              A representative LipoD-Nef fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                               AAY02354 standard; Protein; 326
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                                                                                                                                                                                                                                                                                                                (first entry)
Similarity 78.8
24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-302282/25.
N-PSDB; AAX35690.
                                                                                                                                                                                                                                                                                                                                               HIV nef gene;
                                                                                                                                                                                                                                                                                                                                                                                              WO9916884-A1
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 Local Sim
nes 324;
                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                AAY02354;
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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                              QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPG 241
                                                                                                                                                                                                                                                                                                                                                                                                               242 VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERËVLEWRFDSRLAFH 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI 361
                                                                                                                       63
                                                                                   2 SSHSSNWANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                                                                                        4 sshssnmantgmksdkiiiahrgasgylpehtleskalafaggadylegdlamtkdgrlv
                                                                                                                                                                                                                                                 WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP
Score 1697.5; DB 20; Length 326; Pred. No. 1.1e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a His tagged ProtD-Nef fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----tsghhhhhh 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 SYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 411
                                          Indels
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                                          0; Mismatches
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2000GB-0013806.
2000WO-EP05998.
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  75.3%;
78.8%;
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                                            Conservative
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                                                                                  The present sequence represents a His-tagged ProtD-Nef fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV, Tat, Nef or Nef-Tat and HIV gpl20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein; vaccine; HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                            VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH 301
                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                    61
New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
protein or polynucleotide for the manufacture of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                                                                                                                                                                                                                                                                                                                                                                                              VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPG
                                                                                                                                                                                                                                                                                           Score 1697.5; DB 22; Length 326;
Pred. No. 1.1e-152;
0; Mismatches 0; Indels 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A representative HIV-1 Nef-Tat-His protein.
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                                                        Disclosure; Fig 1; 90pp; English.
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                                                                                                                                                                                                                                                                                            75.3%;
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hes 323; Conservative
                                                                                                                                                                                                                                                326 AA;
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Best Local Si
Matches 323,
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                                                                                                                                                                                                                                                  Sequence
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AAY02351
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The present sequence represents a representative HIV-1 Nef-Tat-His protein. The protein is used in the creation of the Guslon proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                            110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                         QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a His-tagged Nef-Tat linked protein of
                                                                                                                                                                                                                                                               Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                          74.9%; Score 1688; DB 20;
100.0%; Pred. No. 8.2e-152;
tive 0; Mismatches 0;
                                                                                                                          HIV Tat or Nef protein linked to a fusion partner
                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                                                                 Disclosure; Fig 2; 66pp; English.
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98WO-EP06040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 302; Conservative
                                                                  Bruck C, Godart SAG,
                                                                                      WPI; 1999-302282/25.
N-PSDB; AAX35687.
                                                                                                                                                                                                                               302 AA;
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17-SEP-1998;
                     26-SEP-1997;
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| hh 302
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                                                                                                                                                                                                                                Sequence
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Voss WPI;

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The present sequence represents a representative HIV-1 mutant Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 fpdwqnytpgpgvrypltfgwcyklvpvepdkveeankgentsllhpvslhgmddperev 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a His-tagged mutant His protein of HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1675; DB 20;
Pred. No. 1.4e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                   HIV Tat or Nef protein linked to a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 302
                     Synthetic.
Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 99.0
                                                                                                                                                                                                                                             Godart SAG,
                                                                                                                                                                                                                                                                                WPI; 1999-302282/25
                                                                                                                                                                                                           (SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG63239 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                  N-PSDB; AAX35693
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                                                                                                                                         17-SEP-1998;
                                                                                                                                                                          26-SEP-1997;
                                                                      WO9916884-A1
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                                                                                                         08-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tat protein;
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                                                                                                                                                                                                         New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mggkwskssvvgwptvrermrraepaadgvgaasrdlekhgaitssntaatnaacawlea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCFITKALGISYGRKKRRORRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 8.2e-152;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A representative HIV-1 mutant Tat-His protein
                                                                                     SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ниу nef gene; fusion protein; HIV nef
vaccine; HIV infection; protein D.
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                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 90pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.9%; Scillarity 100.0%; P. Conservative 0;
31-JAN-2000; 2000GB-0002200.
14-APR-2000; 2000GB-0009336.
06-JUN-2000; 2000GB-0013806.
28-JUN-2000; 2000WO-EP05998.
                                                                                                                                                      WPI; 2001-476172/51.
N-PSDB; AAH42877.
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Best Local Similarity
Matches 302; Conserv
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AAY02349 standard; Protein; 215
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gp120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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                                                                                                                                                                                                    linked to Tat (Nef-Tat) protein or polynucleotide and an HIV protein or polynucleotide for the manufacture of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
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Pred. No. 1.4e-150;
2; Mismatches 1;
                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                         Disclosure; Fig 1; 90pp; English.
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99.0%;
                  Human immunodeficiency virus
                                                                                        2000GB-0002200.
2000GB-0009336.
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2000WO-EP05998
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                                  WO200154719-A2
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14-APR-2000;
06-JUN-2000;
28-JUN-2000;
                                                                       29-JAN-2001;
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Best Local Simi
Matches 299;
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present sequence represents a representative HIV-1 Nef-His protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
                          fusion protein; HIV nef gene; Nef protein; Tat protein; infection; protein D.
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                                                                                                                  Human immunodeficiency virus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                             or Nef protein linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.5%; 71.2%;
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Matches 215; Conservative
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                                        gene;
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RESULT

RESULT 13 AAY02349 111111 tsghhhh 213

This invention describes novel binding partners (A) (1) for negative factor protein (Nef) that competitively inhibit binding of calmodulin (I) to Nef, or (11) for (I) that competitively inhibit binding of Nef to (I). (A) are used for prevention, diagnosis (by specific detection of intraand/or extra-cellular Nef, including staging of infection), and/or treatment of infections with human immune deficiency virus (HIV). 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169 Binding agents used for treatment, prevention and diagnosis of human immune deficiency virus infection NEF protein; calmodulin; negative factor protein; binding inhibitor; diagnosis; detection; infection; treatment; HIV. **QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY** DB 21; Length 206; Score 1120; DB 21; Pred. No. 4.3e-98; 0; Mismatches 2; Human NEF protein/calmodulin binding inhibitor. lewrfdsrlafhhvarelhpeyfknc 206 AAY50795 standard; protein; 206 AA LEWRFDSRLAFHHVARELHPEYFKNC Antz C; Claim 3; Fig 1; 29pp; German. 49.78; 99.08; 99WO-EP03105 98DE-1020224 (first entry) Conservative Schott M, Schorr J, WPI; 2000-038789/03 Best Local Similarity Matches 204; Conserv 206 AA; (SCHO/) SCHOTT M. (SCHO/) SCHORR J. (ANTZ/) ANTZ C. W09957136-A2 17-FEB-2000 Homo sapiens 06-MAY-1999; 06-MAY-1998; 11-NOV-1999, 410 HH 411 214 hh 215 AAY50795; Sequence Query Match 15 181 170 207 ò g ò g ò g ò g å - 6 Ĥ The present sequence represents a His-tagged Nef protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act. In synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20. MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169 229 289 CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH 409 Gaps 9 New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH 87; Length 215; HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load. Indels Amino acid sequence of a His-tagged Nef protein of HIV DB 22; 0 Score 1139.5; DB 2 Pred. No. 6 4e-100; 0; Mismatches 0; (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS AAG63231 standard; Protein; 215 AA Disclosure; Fig 1; 90pp; English. 2000GB-0002200. 2000GB-0009336. 2000GB-0013806. 50.5%; 71.2%; Human immunodeficiency virus 2001WO-EP00944 28-JUN-2000; 2000WO-EP05998 (first entry) Conservative WPI; 2001-476172/51. N-PSDB; AAH42875. Best Local Similarity Matches 215; Conserv Ä 215 WO200154719-A2 31-JAN-2000; 14-APR-2000; 06-JUN-2000; 29-JAN-2001; 01-OCT-2001 02-AUG-2001 Synthetic Sequence AAG63231; Query Match Voss G; 110 170 230 290 350 61

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AAR38893;

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This invention describes a novel retroviral packing cell (I), comprising the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV coding gene gp, or a part of these. The products of the invention have anti-HIV and cytostatic activity and con be used for gene therapy. (I) is useful for in vitro infection of cells, especially hematopoletic stem cells, for expression of transgenes in cells and as a pharmaceutical carrier for gene therapy. (I) is therefore useful in the treatment of infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and other diseases. This sequence represents the Human immunodeficiency virus (HIV-1) nef protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New retroviral packing cell useful as pharmaceutical carrier in gene therapy for treatment of HIV and neoplasms, comprises retroviral genes
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Pred. No. 1.3e-97;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type
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                                                          AAB10054;
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                                                                                                                                                                                                                                                                                                                     AIDS; antibody; p25; gpl10; gp41; assay; detection;
immunity; vaccine.
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Sabatier JM;
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Pred. No. 1e-97;
0; Mismatches
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                                                                                  AAR38893 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus-1.
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Best Local Similarity 99.0%;
Matches 204; Conservative (
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91US-0754300
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V, Rochat H,
                                                                                                                                                                                                                                                              Nef protein of HIV-1.
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Length 206; Indels

Sequence

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A comparison of AAN60287 with the cDNA of the HTLV-III genome revealed one particular clone, designated p7.11 which contained a DNA sequence encoding this peptide (AAP60308) sequence. This approx 2.2 kilobase covers the precursor gay region and encodes, 5' to 3', p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base pairs 3' to the gay region (see AAN60288).
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                                                                                                                                                                                                                                                                                                        syndrome polypeptide(s) - obtd. by used for dlagnosis and in vaccines
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Pred. No. 3.1e-97;
4; Mismatches 2;
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                            HIV; LAV; AIDS; diagnosis; vaccine
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                                                        HTLV-IIIB/H9 cells (ATCC CRL
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97.1%;
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85US-0805069.
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  Sequence of E' protein
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Best Local Similarity
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04-DEC-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an antigenic composition comprising an isolate primate lentivirus whose genome contains an engineered non-revertible null mutation in the nef gene, or an infectious DNA clone in a carrier. The antigenic composition is used in vaccines against infection by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Lentivirus antigenic compositions - containing lentivirus with nef
gene deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                        Antigenic composition; primate; lentivirus; nef gene; vaccine; infection; AIDS; HIV-1; nef protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1114; DB 20;
Pred. No. 1.6e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches.
                                                                                                                                                  Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2A-R; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 LEWRFDSRLAFHHVARELHPEYFKNC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW89326 standard; Protein; 206
                                                                                                                                                                                                                                                           94US-0188583.
90US-0551945.
91US-0727494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%;
llarity 97.6%;
Conservative
                                                                                                                                                                                                                                 94US-0188583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP61515 standard; Protein;
                                                                               HIV-1 nef protein sequence
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-080408/07
N-PSDB; AAV81866.
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Best Local Similarity
Matches 201; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206
                                                                                                                                                                                                                                                                                                                                             Desrosiers RC;
                                                                                                                                                                                                                                                           27-JAN-1994;
12-JUL-1990;
09-JUL-1991;
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                                                     01-JUN-1999
                                                                                                                                                                             US5851813-A.
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Sequence

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Gaps

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Length 206; Indels 9

AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.

Lymphadenopathy virus

(first entry)

08-JUN-1991

AAP61515;

19

RESULT 1

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This invention describes a novel fusion polypeptide which comprises (a) a first polypeptide sequence of an AIDS associated E', env, or gag polypeptide, that specifically binds complementary antibody and (b) a second polypeptide sequence which is not an AIDS associated virus polypeptide. Also described are are (1) a fusion polypeptide having a herpes simplex virus (HSV) gD signal peptide sequence fused in reading frame with a polypeptide sequence other than HSV gD, (2) a nucleic acid encoding a fusion polypeptide as in (1); (3) an expression vector comprising a nucleic acid as in (2); (4) a host comprising a vector as in (3). The AIDS-associated fusion polypeptides can be used in the detection of and vaccination against viral etiological agents of AIDS. They can also be administered as a pharmaceutical agent to inhibit infection by AIDS associated retrovirus or dissemination of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEBEEVGFPVTPQVPLRPMTYRAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New AIDS-associated fusion poly:peptide(s) - used for the detection of AIDS or to inhibit infection by AIDS associated retrovirus or dissemination of such retrovirus in infected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1092; DB 20;
Pred. No. 2e-95;
1; Mismatches 7;
                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 2A-J; 47pp; English.
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Human lymphotropic virus type III.
                                                                                                                                                                                                            Asp
                                                                                                                                                                                                                                             Val
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96.1%;
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                                                                                                                                       label- Asp,
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93US-0129009.
94US-0282857.
                                                                 'label- Val,
                                                                                                      label= Thr,
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84US-0685272
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88US-0227568
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Matches 198; Conservative
                                                                                                                                                                         label-
                                                                                                                                                                                                            label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                             Misc-difference 153
                                                                                                                                                      Misc-difference 65
                                                                                     Misc-difference 5
                                                                                                                     Misc-difference 5.
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                                                                                                                                                                                         Misc-difference
                                                Misc-difference
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24-DEC-1984;
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDS; acquired immunodeficiency syndrome; viral infection; env protein; fusion polypeptide; E' protein; aga protein; pol protein; P' protein; gD signal peptide; detection; vaccination; etiological agent; infection inhibitor; AIDS associated retrovirus; p24; gp41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
                                                                                                                                                                                                                                                                                                                                       antibodies against lymphadenopathy virus and useful in detecting AIDS antibodies or in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The inventors claim a polypeptide which is recognised by sera of human origin contg. antibodies against the virus of lymphadenopathies (LAV) or acquired immune deficiency syndrome (AIDS). Also claimed are various peptides corresp. to the AA sequences deducible from proteins encoded by LAV DNA, defined by specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance with a formula given in the specification.
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                                                                                                                                                                                                                             Montagnier L, Krust B, Chamaret S, Clavel F, Chermann J-C;
Barre-Sinoussi F, Alizon M, Sonigo P, Stewart C, Danos O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.1%; Score 1107; DB 7; 98.1%; Pred. No. 7.9e-97; Live 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW90179 standard; Protein; 206
                                                                                                                                                                         CENT NAT RECH SCI
                                                                                                  85GB-0001473.
84FR-0016013.
84GB-0029099.
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                                                                                                                                                                                             ) INST PASTEUR
                                                                                                                                                                                                                                                                                                   WPI; 1986-119166/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 202; Conserv
                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN60365
                                                                                                                                                                                                                                                                Wain-Hobson S;
                                                                                                                                                                         (CNRS ) CNRS (INSP ) INST
                                                                                                                      18-OCT-1984;
16-NOV-1984;
                                                                  18-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1999
                                                                                                      21-JAN-1985;
WO8602383-A
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                                 24-APR-1986
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Query Match

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230 131 290 191

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Sequence

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Length 206; Indels

AAW90179

AAW90179
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AC AAW9
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KW AIDE
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KW GSJ
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Best Local Similarity 83.8 Matches 181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful contained and a negative is esponse against infection or disease caused by virulent strains of HIV, response against infection or disease caused by virulent strains of HIV, referably human. It is also useful for lowering transmission rate to previously uninfected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human immunodeficiency virus-1 (HIV-1) Jifl Nef protein. The different codon optimised nef constructs of the invention are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                        DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; mutant; mutein.
230 FPDWQNYTPGPGVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
            /note= "Myristylation site"
                                                                                                                                                                                                                                                                         Location/Qualifiers
2
                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1
                                         290 LEWRFDSRLAFHHVARELHPEYFKNC 315
                                                      AA.
                                                                                                                   AAE04960 standard; Protein; 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 13; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                            99US-0172442
                                                                                                                                                                                                                                                                                                                                                                      15-DEC-2000; 2000WO-US34162
                                                                                                                                                               (first entry)
                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     Liang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-417878/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA;
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                                                                                                                                                                                   HIV-1 jrfl Nef
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-1999;
                                                                                                                                                                                                        DNA vaccine;
cell mediate
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                                                                                                                                                                                                                                                             Synthetic
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This sequence represents a protein of unspecified function contained in a complete nuclectide sequence of ARV-2 derived from partial sequences of several ARV clones. The invention provides a method for construction of a vector for expression of a polypeptide in a mammalian cell, comprising a polypeptide coding sequence operably linked downstream of an enhanced promoter. The enhanced promoter comprises the human cytomegalovirus immediate early region (HCMV IEL) promoter. The polypeptide can be any of the to the 3' end of the HCMV IEL promoter. The polypeptide can be any of the HIV recombinant polypeptides and especially HIV gpl20. Expression of HIV gpl20 by COS 7 cells transfected with pcWVea containing the above enhanced promoter,
                                          1;
                                                                                                                                                                                                                                                                                110 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 159
                                                                                                                                                                       160 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 219
                                                                                                                                                                                                                                                          DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 279
                                                                                                           Gaps

    comprising cytomegalovirus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein 6 contained in a complete ARV-2 nucleotide sequence.
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                                            Indels
Pred. No. 1e-87;
                                                                                                                                                                                                                                                                                                                                               280 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 315
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                                                                                                                                                                                                                                                                                                                                                                     Enhanced promoter for gene expression
immediate early promoter plus intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 4C-P; 99pp; English.
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  83.8%; Fig. 7.
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85US-0696534.
85US-0773447.
92US-0931191.
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94US-0288336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chapman BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1998
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17-AUG-1992;
28-JUN-1993;
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10-AUG-1994;
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                                          181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; AIDS.
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Shiver JW, Liang X,
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N-PSDB; AAD09605.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                          CRL 8597)
                                                                                                                                                                                                                                                                                                           AAE04962
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                                                                                                      Query Match
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                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the improvement of HIV-1 immunoassays by the use of an HIV-1 antigen comprising an immunogenic fragment of recombinant or synthetic HIV-1 pol, which is encoded by an approximately 9.7 kb sequence between a Bitzi restriction site at position 3006 and an Ndel site at position 5131 of the genome (the proviral DNA sequence is
                                                                                                                                                                                                                                                                                                                           pol fragment; p31; recombinant; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoassay for antibodies against human immune deficiency virus, for diagnosing infection, uses an immunogenic fragment of the pol protein as antigen -
                                                                                                                       WLEAGEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 225
                                                                                                                                MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 165
                                                                    Gaps
                                                                                                     9
 compared with the use of a vector
                                                                                               TOGYFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                    Length 210;
                                                                                                                                                                                                                                                                                                                                                      !uman immunodeficiency virus type 1 'ATCC CRL 8597'
                                                   44.2%; Score 997; DB 19;
85.2%; Pred. No. 2.1e-86;
                                                                                                                                                                                                                                                                                                           CRL 8597) ORF #3-encoded protein.
                                                            Pred. No. 2.1e
16; Mismatches
                                                                                                                                                                                                    EREVLEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 40-P; 99pp; English.
is increased by a factor of 50-100 containing the SV40 early promoter.
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                                                                                                                                                                                                                                                        Protein; 210
                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0089407.
87US-0138894.
92US-0931154.
84US-0667501.
85US-0696534.
85US-0773447.
                                                                                                                                                                                                                                                                                                                           HIV-1; immunoassay; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                         95US-0443434
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-170256/15.
N-PSDB; AAZ90201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                        standard;
                                                           Best Local Similarity
Matches 179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-1995;
                                                                                                                                                                                                                                                                                          22-MAY-2000
                                                                                                                                                                                                                                                                                                           HIV-1 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-1985;
06-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                      US6013432-A
                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1984
                                                                                                                                                                                                                                                                                                                                      detection.
                                                                                                                                                                                                                                                       AAY77299
                                                                                                                                                                                                                                                                        AAY77299;
                           Sequence
                                                    Query Match
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given in AA290201). The immunogenic pol fragment is not immunologically cross reactive with human T cell lymphotropic viruses I or II. The invention also encompasses the used of p31 as an antigen. The recombinant antigens may be produced in Escherichia coll, Saccharomyces cerevisiae or in mammalian cells. Immunoassays using the recombinant HIV proteins may be used to diagnose and stage HIV-1 infections. Sequences
AAY77284-Y77299 represent proteins encoded by the genome of HIV-1 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note- "Wild type myristylation site at Gly2 substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type dileucine motif (Leu-Leu) substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; jrfl Nef; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 165
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                                                                                                                                                                                                                                                                                                         44.2%; Score 997; DB 21; Length 210; 85.2%; Pred, No. 2.1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1 jrfl Nef (G2A, LLAA) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 EREVLEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with Ala-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US34162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with Ala"
174..175
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                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 85.2
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERI ) MERCK & CO INC
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                                                                                                                                                             expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (vytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individual, so as to prolong the asymptomatic phase of the invention are used in the exemplification of the
Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to a DNA vaccine comprising a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
44.2%; Score 996; DB 22;
Best Local Similarity 82.0%; Pred. No. 2.8e-86;
Matches 178; Conservative 16; Mismatches 13;
                                                                                                        Page 18; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                        Claim 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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Gaps

; 9

Indels

Length 210;

110 MGGKWSKSSVVGWPTVRERMRRA----EPAADGVGAASRDLEKHGAITSSNTAATNAAC 164

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Query Match
43.6%; Score 983; DB 12;
Best Local Similarity 82.5%; Pred. No. 4.6e-85;
Matches 174; Conservative 22; Mismatches 9;

210 AA;

Sequence

proteins)

**AWLEAGEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSGRRQDILDLWIY** 

165

HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 

225

61

This sequence constitutes the ORF P protein constituent of a new strain of HTV-1 retrovirus, OYI. This mutant retroviral strain is useful in an assay for diagnosing HIV infection. See also AAQ11943 (OYI nucleotide sequence), AAR12255-61 (other HIV OYI constituent

human retrovirus - is mutant of HIV-1 having istics of HIV-1 OYI, used in diagnosis of HIV infection

WPI; 1991-177518/24.

characteristics of

Purified

8; 23pp; English

Disclosure; fig

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DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL
                                             HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNCT 316
                                   280
220
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HIV-1 strain OYI open reading frame (ORF) F protein
           AAR12262 standard; Protein; 210
                                   (first entry)
                                                           retroviruses
                                                           AIDS;
                                                                       Homo sapiens
                                                                                                         28-OCT-1987;
                                   20-AUG-1991
                                                                                  JS5019510-A
                                                                                              28-MAY-1991
                       AAR12262;
                                                          HIV-1;
26
      AAR12262
RESULT
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Delaporte E,

Wain-Hobson S, Huet T, (INSP ) INST PASTEUR

87US-0113655

28-OCT-1987;

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anti-HIV;
Human tPA leader peptide-HIV-1 jrfl Nef (opt tpanef) mutant protein.
                                                                                                                                                                                                                                                                                                      DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-Hi cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; human; jrfl Nef; opt tpanef; tissue plasminogen activator; tPA; chimeric protein; mutant; muteln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (6-216aa) protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..26
/label- Leader_peptide
/note- "Human tissue plasminogen
lader sequence"
27..237
/note- "Mature HIV-1 Nef (6-216aa
                                                                                                                                                                                                                                                                                                                                                                                             - Human immunodeficiency virus type 1. - Homo sapiens.
                                             195..196
/label= Dileucine_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                        Ź
                                                                                                                                                                      AAE04961 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0172442
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200143693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999;
                                                                                                                                                                                                                                       10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
Chimeric
                                                                                                                                                                                                      AAE04961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                285
                                                                                   180
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                                                                                                                                                       AAE04961
                                                                                                                                   RESULT
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Human immunodeficiency virus type
 Homo sapiens.

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Chimeric
                                                      Key
Peptide
                                                                                                                                                  Protein
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Matches
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                                                                                                                                                                                                                                                                     The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, corrected individual, so as to prolong the asymptomatic condition. The present sequence is human tissue plasminogen activator (HPA) leader peptide-human immunodeficiency virus-1 (HIV-1) if IN Nef (opt tpanef) chimeric multant protein. The mutation include deletion of the myristylation site (Gly2) in the HIV-1 jifil Nef protein.
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                                                                                                                                          Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency vitus-1; HIV-1; human; jrfl nef; opt tpanef; tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 SKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAATNAAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tPA leader peptide-HIV-1 jrfl Nef (LLAA) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.4%; Score 978; DB 22; Length 237; 83.4%; Pred. No. 1.6e-84; tive 15; Mismatches 10; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEREVLEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n the exemplification of the invention.
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                                                                                                                                                                                                                                       Claim 29; Page 17; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE04963 standard; Protein; 237
                                                    Liang X, Fu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.4%
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                     WPI; 2001-417878/44.
               (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AA;
                                                                                                           N-PSDB; AAD09604
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                                                  Shiver JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225
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loads within an infected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human tissue plasminogen activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1) if Nef (LLAA) chimeric mutant protein. The different codon optimised nef constructs of the invention are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a DNA vaccine comprising a DNA reading frame encoding a New Procession vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cyctoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral
                                                                                                                                                                                                                                                                     /note- "Wild type dileucine motif (Leu-Leu) substituted with Ala-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/label- Leader_peptide
/note= "Human tissue plasminogen activator (tPA)
leader_sequence"
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                                                                                                                                                                     27 .237
/note= "Mature HIV-1 Nef (6-216aa) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%; Score 968; DB 22; 82.5%; Pred. No. 1.5e-83; Live 15; Mismatches 12;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 29; Page 19; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0172442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-2000; 2000WO-US34162
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                                                                                                                                                                                                                                 Misc-difference 195..196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shiver JW, Liang X,
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N-PSDB; AAD09606.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               WO200143693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2001
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antiviral;

/note= "Xaa represents a stop codon"

Location/Qualifiers 1.3025 /label= Xaa

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Infection; diagnosis; human; humoral immune response; antiv
cellular immune response; vaccine; treatment; gene therapy
                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                      AAB86169 standard; Protein; 3025 AA.
                                                                                                                                                      HIV-1 subtype C protein fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2000; 2000DE-1056747
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 DE10056747-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-NOV-1999;
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Best Local Simi
Matches 175;
                                                                                                                21-AUG-2001
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                                                                          AAB86169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAO/)
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                    AAB86169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, viz, vpr, vpu, agg, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type I useful for detecting and treating AIDS comprises a specific nucleotide sequence
                                                                                                                                                                                                                                                                                     immunodeficiency virus; non-subtype B; gag; pol; env;
t; tat; rev; nef; vaccine.
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Pred. No. 3.9e-82;
1; Mismatches 15;
                                                                                                                                                                                                                                               HIV-1 non-subtype B clone 962M651-8 nef protein.
PEREVLEWRFDSRLAFHHVARELHPEYFKNC 315
                      Human immunodeficiency virus type 1.
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81.1%; Pre
tive 24;
                                                                                                                                AAB69363 standard; Protein; 206
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                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                         vpu; vif; vpr;
                                                                                                                                                                                                                                                                                                                                                                               WO200026416-A1
                                                                                                                                                                                                                                                                                       human
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                                                                                                                                                                                                                                                                                   HIV-1;
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285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunodeficiency virus type isubtype C/B' which can be used for the induction of specific humoral and cellular immune responses. (1) and pulpapelides (II) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus-1 (HIV-1) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions specific for intersubtype C/B' of HIV-1 so are useful in regions. The products of the invention have antiviral activity. This sequence represents a procein encoded by the HIV-1 subtype C genome described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polynucleotide isolated from human
                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3025;
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                                                                                                 GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
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70.6%; Pred. No. 4.4e-80;
iive 22; Mismatches 42
                                                                                                                                                                  Graf M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                                                  Shao Y,
99DE-1055089
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                                                                                                                                                                                                                                                                N-PSDB; AAH20870
                                                                                                                                                                                                                                                                                                                                     New nucleic acid
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<sup>343</sup> CKKCCFHC 350

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Search completed: August 26, 2002, 08:12:27 Job time: 236 sec

Sequence 43, Appl Sequence 1, Appli Sequence 16, Appli Sequence 15, Appli Sequence 4, Appli Sequence 4, Appli Sequence 17, Appli

Sequence 27, Sequence 27, Sequence 27, Sequence 27,

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170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCES AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.5%; Score 1138; DB 4;
88.7%; Pred. No. 9.6e-107;
iive 2; Mismatches 25;
         US-09-079-587-43
US-08-505-210-1
US-08-09-333-1
US-08-09-33-1
US-08-05-079A-15
US-08-05-079A-15
US-08-05-079A-15
US-09-256-490-4
US-09-256-490-4
US-09-030-613-17
US-09-030-613-17
US-08-09-13-921-1
US-08-09-128A-27
US-08-094-128A-27
US-08-455-992-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                      Sequence 76, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
TITLE OF INVENTION: Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQ
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 76
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
COTATION: (1)..(239)
COTHER INFORMATION: X os selenocysteine.
US-08-679-493A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.7°
Matches 211; Conservative
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US-08-388-353-644
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                                                                              Search time 38.46 Seconds (without alignments) 261.022 Million cell updates/sec
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1 CSSHSSNWANTQMKSDKIII......QSRGDPTGPKETSGHHHHHH 411
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-679-493A-75
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US-09-485-885-23
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US-09-485-885-1
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US-09-485-885-1
US-09-485-885-1
US-09-485-885-1
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                                                                                                                                                                                                                   231628 segs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                              2002, 08:10:39
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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230 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; ' Indels
                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-010-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
  NON-PATHOGENIC STRAINS OF HIV-1
841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1115; DB 3;
Pred. No. 1.6e-104;
1; Mismatches 3;
                                                               E: SCULLY, SCOTT, MURPHY & PRESSER 400 GARDEN CITY PLAZA
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; Sequence 75, Application US/08679493A
Patent No. 6303295
; GENERAL INFORMATION:
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 644:
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Best Local Similarity 98.1%;
Matches 202; Conservative
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LENGTH: 206 amino acid
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                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                 STREET: 400 GARDE CITY: GARDEN CITY
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                                                                                                                    STATE: NEW YORK COUNTRY: U.S.A. ZIP: 11530-0299
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                                                               ADDRESSEE:
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                                                                                                                    APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14 FEB-1995
CLASSIFICATION: 424
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49.4%; Score 1115; DB 3;
Best Local Similarity 98.1%; Pred. No. 1.6e-104;
Matches 202; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                    ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 644, Application US/08488551B Patent No. 6015661
GENERAL INFORMATION:
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Patent No. 6010895
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4346
TELEX: 230 901 SANS UR
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
STRANDEDNESS:
                                                               Deacon, Nicholas J.
Learmont, Jennifer C.
McPhee, Dale A.
Crowe, Suzanne
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APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              New York
: United States
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APPLICANT:
APPLICANT:
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Length 206;

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122 WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATN--AACAW----LEAQEEEEV 175
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                                                                                                                                    61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTGGY 120
                                       110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG 121
     Gaps
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                                                             1 MGGKWSKSSVVGWPAVRERMRRAEPAADGVGAASRDLEKHGAITSSVTAANNADCAWLEA
                                                                                                                  QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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   Indels
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Pred. No. 6e-51;
6; Mismatches 73;
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILE OF INVENTION: Vaccine
FILE REFERENCE: B42107
CURRENT FLING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US/09/485,885
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQ ID NOS: 23
FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
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36.0%;
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Best Local Similarity 36.0
Matches 155; Conservative
   Conservative
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US-09-485-885-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID
SOFTWARE: FastSE
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FPD 123
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   120;
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LENGTH: 278
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APPLICANT:
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 R-LLPDWQNYTPGPGVRXPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPE 177
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9
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                                                                                                                                                                                                                                                                                                                                                                                                         15;
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Pred. No. 5.3e-90;
2; Mismatches 15
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Pred. No. 9.3e-57;
                                                                                                                                                                                                           ORGANISM: Human immunodeficiency virus type 1
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CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
NUMBER OF STO
CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT FILING DATE: 1996-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 REVLEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                             NAME/KEY: VARIANT
COTATION: (1)..(206)
COTHER INFORMATION: X is selenocysteine
US-08-679-493A-75
             CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
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KLIMA, Annelies
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89.08;
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TRKOLA, Alexandra
PREDL, Renate
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BUCHACHER, Andrea
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Best Local Similarity 89.0
Matches 186; Conservative
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MUSTER, Thomas
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APPLICANT: MUSTER, T
TITLE OF INVENTION:
FILE REFERENCE: 193
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Best Local Similarity
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LENGTH: 206
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APPLICANT:
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APPLICANT:
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APPLICANT:
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US-09-485-885-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 VDLSHFLKEKGGLEGLIHS---QRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGW 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 CYKLVPVEPDKVEEANKGENTSLLH---------PVSL---HGMDDPERE 288
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----ASQQTSGHH 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 ------KWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITS---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDE--IDGVNHQHLPARRAEPQRHTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.7%; Score 579; DB 4; Length 383;
llarity 34.5%; Pred. No. 4.4e-50;
Conservative 21; Mismatches 118; Indels 178;
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APPLICANT: Cabazon Silva, Teresa
APPLICANT: Cabazon Silva, Teresa
APPLICANT: Cabazon Silva, Teresa
APPLICANT: Combardo Sencheith, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45.107
CURRENT APPLICATION: NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
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                                                                                                                                          Sequence 23, Application US/09485885 Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo sapien US-09-485-885-23
                      11111111
269 -VTSGHHHHHH 278
401 KETSGHHHHHH 411
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Best Local Similarity
Matches 167; Conserv
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64 VIHDHFILDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMAMHGDT----- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 61
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Pred. No. 3.9e-50;
9; Mismatches 27
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Dese, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Benchetikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION NUMBER: B4507-08-28
PRIOR FILING DATE: 1998-08-17
PRIOR PLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                        APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo Garcherine Marie Ghislaine
APPLICANT: Lombardo Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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Sequence 8, Application US/09485885
Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.5%;
Best Local Similarity 66.5%;
Matches 123; Conservative
                                                                                                Bruck, Claudine
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapien
US-09-485-885-8
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US-09-485-885-1	Db 148H0H0
Ouery Match 25.5%; Score 575; DB 4; Length 220; Best Local Similarity 66.5%; Pred. No. 4.9e-50; Matches 123; Conservative 9; Mismatches 27; Indels 26; Gaps 3;	
Qy 2 SSHSSNWANTOMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 61 	Oy 361 ISYGRKRRORRPPQGSQTHQVSLSKOPTSQSRGDPTGPKETSGHHHHHH 411 Db 215ASQQTSGHHHHHH 227
OY 62 VIHDHELDGLTDVAKKEPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG 121	RESULT 11 US-09-485-885-6 ; Sequence 6, Application US/09485885
QY 122 WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP 181	; Patent No. 634224 ; GENERAL INFORMATION: ; APPLICANT: Bruck, Claudine ; APPLICANT: Cabezon Silva, Teresa
Qy 182 QVPLR 186   1   Db 158 AEPDR 162	; APPLICANT: Delisse, Anne-Marie Eva Fernande ; APPLICANT: Gerard, Catherine Marie Ghislaine ; APPLICANT: Lombardo-Bencheikh, Angela ; TITLE OF INVENTION: Vaccine
RESULT 10 US-09-485-885-16 Sequence 16. Application IS/00485885	; FILE REFRENCE: B45107 ; CURRENT APPLICATION NUMBER: US/09/485,885 ; CURRENT FILING DATE: 2000-02-18 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
Patent No. 63 GENERAL INFOR APPLICANT: APPLICANT:	FRIOR FILING DATE: 1998-08-1/ FRIOR FILING DATE: 1997-08-22  FUNDER OF SEQ ID NOS: 23  FORTHARDER FEEL TO SEE TO NOS: 23
; APPLICANT: Delisse, Anne-Marie Eva Fernande ; APPLICANT: Gerard, Catherine Marie Ghislaine ; APPLICANT: Lombardo-Benchelkh, Angela ; TITLE OF INVENTION: Vaccine	6 371 Homo sapien
FILE REFERENCE: B45107 CURRENT APPLICATION NUMBER: US/09/485,88 CURRENT FILING DATE: 2000-02-18	9-
PRIOR APPLICATION NUMBER: PCT/EP98/05285 PRIOR FILING DATE: 1998-08-17 PRIOR APPLICATION NUMBER: GB 9717953.5 PRIOR FILING DATE: 1997-08-22	Query Match 25.4%; Score 572; DB 4; Length 371; Best Local Similarity 34.5%; Pred. No. 2.1e-49; Matches 164; Conservative 27; Mismatches 112; Indels 172; Gaps 1
$\sim$	Qy 2 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEODLAMTKDGRLV 61
; TYPE: PRT ; ORGANISM: Homo sapien US-09-485-885-16	QY 62 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG 121
Query Match 25.4%; Score 572; DB 4; Length 227; Best Local Similarity 36.5%; Pred. No. 1e-49; Matches 150; Conservative 14; Mismatches 59; Indels 188; Gaps 10;	OY 122 WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP 181
YLPEHTLESKALAFAQQADYLEQDLAMTKDGRI 	QY 182 OVPLRPWTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYF 230
Qy 62 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIOSLEMTENFETWGGKWSKSSVVG 121	QY 231 PDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVL 290
SEEEVGFPVTP     NE	QY 291 EWRPDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNC 341
ORRODILDLWIYHTQGYFPDWQNYTPGPG 24	Oy 342 YFIT 356
242 VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH	QY 357 KALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 411 

Gaps 14;

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; ORGANISM: Homo sapien
US-09-485-885-19
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SEQ ID NO 19
LENGTH: 227
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APPLICANT: Bruck, Claudine
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Patent No. 6342224
                                                                                                                                   Sequence 4, Application US/09485885 Patent No. 6342224
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Best Local Similarity
Matches 149; Conserv
                                                                                                              GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lombardo-Bencheikh, Angela TITLE OF INVENTION: Vaccine
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SOFTWARE: FastSEQ for Windows Version
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                                                      APPLICANT:
                                                                                             APPLICANT:
              APPLICANT:
                               PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP 181
                                                                                                                                                                                                                                                                                                361 ISYGRKKRRORRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 411
                                                                                                                                                                                                                                                                                                                                       162 LPARRAEPQRHTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWC---
                                                                                                                                                                                                                                                                                                                                                                             302 HVARELHPE-YFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPG 241
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INVENTION:
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                 Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                                                                             Bruck, Claudine
                Lombardo-Bencheikh, Angela
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                                                                                                                                                                                                                                                          --ASQQTSGHHHHHH
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SOFTMARE: FASTSEQ for W
SEQ ID NO 4
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-4
                                             PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
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US-08-679-493A-74
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Best Local Similarity
                                                                                                                                                                                                                                                                                   Sequence 74, Application US/08679493A
Patent No. 6303295
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/485,885 CURRENT FILING DATE: 2000-02-18 PRIOR APPLICATION NUMBER: PCT/EP98/05285 PRIOR FILING DATE: 1998-08-17 PRIOR APPLICATION NUMBER: GB 9717953.5 PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                                                                               APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT FILING DATE: 1996-07-12
ORGANISM: Human
                                  ENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHH 410
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immunodeficiency virus
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type
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; STRAIN:
US-08-450-257-1
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                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: FAWELL, Stephen E.
APPLICANT: TAT-DERIVED TRANSPORT POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Datentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/OR /***
FILING DATE:
                                                                                                           22.1%; Score 498.5; DB 4;
llarity 73.0%; Pred. No. 1.5e-42;
Conservative 4; Mismatches 7;
                                                                                                                                                                                                                                        170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGG----
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APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(151)
; OTHER INFORMATION: X is selenocysteine.
US-08-679-493A-74
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28-APR-1994
NUMBER: US 07/934,375
21-AUG-1992
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28-JUL-1993
IMBER: PCT/US93/07833
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REGISTRATION NUMBER: 27,794
REFRENCE/DOCKET NUMBER: B170 CIP
TELECOMMUNICATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JABER: US 08/158,015
24-NOV-1993
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Patent No. 5652122
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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APPLICATION NUMBER: U
FILING DATE: 28-APR-1
APPLICATION NUMBER: U
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                                                                                                             Query Match
Best Local Similarity
Matches 103; Conserv
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318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPDG 377
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                                                                                                                                                                                                                                                                                                                    Length 86;
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APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
IITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/08/450,246 FILING DATE: 25-MAY-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                    Score 486; DB 1; I
Pred. No. 1.2e-41;
0; Mismatches 0;
                                                                                                                                                                                                        human immunodeficiency virus
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APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUC-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/459,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
FILING DATE: US 07/934,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/158,015
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COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08450246
Patent No. 5670617
                                                                                                                                                                                                                                                                                                                    Query Match
21.6%; Sc
Best Local Similarity 100.0%; P
Matches 85; Conservative 0;
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TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR EGG ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Haley Jr., James REGISTRATION NUMBER: 27
                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
FILING DATE: 02-JA
                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                             type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                      Length 86;
                                                                                                                                                                                                                                                                                                                                                                            Indels
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APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, Janes G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                         Score 486; DB 1; 1
Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                          ; ORGANISM: human immunodeficiency virus
STRAIN: type 1
US-08-450-246-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US93/07833
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APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US 08/158,015
24-NOV-1993
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02-JAN-1991
    B170 CIP
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08450098 Patent No. 5674980
                                   TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
REFERENCE/DOCKET NUMBER: B
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                    Query Match 21.6
Best Local Similarity 100.
Matches 85; Conservative
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-JAN
APPLICATION NUMBER:
FILING DATE: 24-NOV
                                                                                                                                                               amino acid
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318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI$YGRKKRRQRRRPPQG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 86;
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APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: PEPINSKY, R. B.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FTIING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    21.6%; Score 486; DB 1; I
100.0%; Pred. No. 1.2e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                              אני איט human immunodeficiency virus
STRAIN: type 1
US-08-450-098-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-ANG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-ANG-1993
APPLICATION NUMBER: US 07/454,450
APPLICATION NUMBER: US 07/454,450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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21-DEC-1989
MBER: US 07/636,662
NAME: HALGY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08451233 patent No. 5747641
                                                                                TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 85; Conserv
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 486; DB 1; 100.0%; Pred. No. 1.2e-41; tive 0; Mismatches 0;
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FILING DATE: 19911213
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REPRENCE/DOCKET NUMBER: 8255-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-808-452-1
; Sequence 1, Application US/07808452
; Patent No. 6063612
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Best Local Similarity 100.(
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19
CLASSIFICATION:
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US-08-450-236-1
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9 PF
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Patent No. 5804604
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: FAREL, Stephen E.
APPLICANT: FARELL, Stephen E.
APPLICANT: FERRILL, Stephen E.
APPLICANT: FERRILL, TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
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100.0%; Pred. No. 1.2e-41;
ilve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: human immunodeficiency virus ; STRANISM: type 1 US-08-451-233-1
FILING DATE: 02-JAN-1991
FILING DATE: US 08/158,015
FILING DATE: US -ANOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9000
TELEPAN: (212) 596-9010
TELEPAN: (212
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STREET: 1251 Avenue of the Americas
CIIY: New York
STATE: New York
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Best Local Similarity 100.
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-08-450-236-1
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0; Gaps

Length 86; 0; Indels

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APPLICAL...
FILING DATE: 21-DEC-126,
APPLICATION UNBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION UNBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Habey Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFEX: (4-8367
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
TELEFAX: (212) 596-9090
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2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPPQG 61
                                                                                                                                                                                                                                                                                        BALLAUN, Claudia
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; ORGANISM: Homo sapien
US-09-451-905-19
                                                                                                                                                                                                               GENERAL INFORMATION:
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LENGTH: 86
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Floridwicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                     the sequence of the TAT protein of HIV-1
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FILLING DATE: US/09/030,613 FILLING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.6%; Score 486; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.2e-41;
Matches 85; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                             21.6%; Score 486; DB 3; 1
100.0%; Pred. No. 1.2e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                                                                                                                                                                                                                                                                                                                                      62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
TYPE: AMINO ACID
TOPOLOGY: 14-7
OLDFORM
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 85; Conservative
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     SEQUENCE CHARACTERISTICS
                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                   INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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STATE: Washington
COUNTRY: USA
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STRANDEDNESS:
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STREET: 630
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US-09-030-613-19
                                                                                                               ANTI-SENSE:
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318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGįSYGRKKRRQRRRPPQG 377
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FILE REFERENCE: 200124.4025 FOR IDENTIFYING AND USING THE SAME
FILE REFERENCE: 200124.4024.405 FOR IDENTIFYING AND USING THE SAME
CURRENT APPLICATION NUMBER: US/09/451,905
NUMBER OF SEQ ID NOS: 48
SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTHARE: FASTER SOFTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
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; Sequence 19, Application US/09451905
; Patent No. 6306613
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APPLICANT: Robert Z. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
ITILE OF INVENTION: MODULATORS OF I
TITLE OF INVENTION: AND METHODS FOR
FILE REFERENCE: 200124.402C4
                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09124900
Patent No. 6268484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PURISCHER, Martin
TRKOLA, Alexandra
PREDL, Renate
SCHMATZ, Christine
KLIMA, Annelies
STEINDL, Franz
MUSTER, Thomas
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BUCHACHER, Andrea
ERNST, Wolfgang
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318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 377
                                                                                                                                  318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 377
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                                                                                                                                                          2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPGG 61
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                                      Length 86;
                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9210770
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                        21.6%; Score 486; DB 4; I
100.0%; Pred. No. 1.2e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                    62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
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T: 333 Ravenswood Avenue
Menlo Park
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: P'-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 859-4550
TELEFAX: (415) 859-3880
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 86 amino acids
AMINO ACID
                                                                Best Local Similarity 100.0
Matches 85; Conservative
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INDIVIDUAL ISOLATE:
PCT-US92-10770-1
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Best Local Similarity
Matches 85; Conserv
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PCT-US92-10770-1
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                                             Query Match
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                                                                    Gaps
                                                                                                                                  2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPGG 61
                Score 486; DB 4; Length 86;
Pred. No. 1.2e-41;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABCOW, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TILE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Felease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/45,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILEPHONE: (212) 596-9000
TELEPANICATION INFORMATION:
TELEPANICATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELEPANICATION INFORMATION:
TELEPANICATION OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
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STRAIN: type 1
US-08-235-403-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
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21.6%; Scu.
100.0%; Pre
0;
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Patent No. 6316003
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                                                                85; Conservative
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                   Query Match
Best Local Similarity
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COUNTRY: USA
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175 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43. Application US/08816155B
Patent No. 5990091
CENERAL INFORMATION:
CENERAL INFORMATION:
COX, WILLIAM I.
APPLICANT: GETTIC, RUSSELL R.
APPLICANT: MARTHEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
TITLE OF INVENTION: MITHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                      Length 266;
                                                                                                                                                                                                                                                                                                                                            Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                Score 478.5; DB 3;
Pred. No. 3.5e-40;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: FROMMER LAWRENCE & HAUG LLP 745 FIFTH AVENUE
                          INVENTION: MAKING AND USES THEREOF
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NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
                   TITLE OF INVENTION: MAKING AND USES THEREE PILE REFERENCE: 454310-3010
CURRENT APPLICATION NUMBER: US/08/815,809
CURRENT FILING DATE: 1997-03-12
                                                                                                                                                                                                                                                                                                21.2%;
ilarity 77.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO:
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LENGTH: 280 amino acid
                                                                                                                                                                    ; TENGTH: 266
; TYPE: PRT
: ORGANISM: Vaccinia virus
US-08-815-809-5
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                                                                                                        NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver.
SEQ ID NO 5
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STRANDEDNESS: n/a
TOPOLOGY: linear
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Best Local Similarity
Matches 92; Conserv
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US-08-816-155B-43
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                                                                                                                                APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
CORRESONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                              E: Howson and Howson
Spring House Corporate Cntr, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 486; DB 5; 1
Pred. No. 1.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                   Sequence 2, Application PC/TUS9506077 GENERAL INFORMATION:
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62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
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REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IRI4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
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Patent No. 6004777
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
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100.0%;
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APPLICANT: GOBBEL, Scott J.
APPLICANT: COX, William I.
APPLICANT: GETTIG, Russell R.
APPLICANT: PINCUS, Steven E.
APPLICANT: PACOESTI, Enzo
APPLICANT: JACOES, BETTERM L.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Pennsylvania
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Best Local Similarity
Matches 85; Conserv
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PCT-US95-06077-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                              RESULT 26
PCT-US95-06077-2
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APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
210 NYTPGPGVRYPLTFGWCYKLVPM----IETV------PVKLKPGMDGP--KVKQW 252
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA:-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,210
FLING DATE: 14-AdG-1995
PROOR APPLICATION NUMBER: US 08/215,248
FILING DATE: 21-MAR-1994
PROOR APPLICATION NUMBER: US 08/215,248
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,373
REGISTRATION NUMBER: 40,373
REGISTRATION NUMBER: 40,373
REGISTRATION NUMBER: 017753-066
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6020
TELEPHONE: (703) 836-6020
TELEPHONE: (703) 836-6020
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                                                                                                                                                                                                                                                                            US-08-505-210-1; Sequence 1, Application US/08505210; Patent No. 5981258; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                          a
                                                                                                                                                                                                                                                                                                                                            175 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 NYTPGPGVRYPLTFGWCYKLVPM----IETV------PVKLKPGMDGP--KVKQW 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TARRAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: COX, WILLIAM I.
APPLICANT: COX, WILLIAM I.
APPLICANT: CETTIG, RUSSELL R.
APPLICANT: PACLETTI, ENZO
APPLICANT: PACLETTI, ENZO
APPLICANT: PACLETTI, ENZO
APPLICANT: PACLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: WETHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
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APPLICATION NUMBER: US/09/079,587
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Pred. No. 3.7e-40;
4; Mismatches 6;
                                                          DB 2;
                                                    Score 478.5; DB 2
Pred. No. 3.7e-40;
4; Mismatches 6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSCTWARE: PatentIn Polocial Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Companion of the Com
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Patent No. 6130066
GENERAL INFORMATION:
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Best Local Similarity 77.3%;
Matches 92; Conservative
                                                    Query Match 21.2%;
Best Local Similarity 77.3%;
Matches 92; Conservative
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                                                                                                                       STRAIN: Lai INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1 US-08-505-210-1
                                                                                                                                                                                                                                  Score 470; DB 2; Length 86;
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175 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 234

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235 NYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH-GMDDPEREVLEW 292

86 amino acids

Search completed: August 26, 2002, 08:10:40 Job time: 129 sec

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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency; phosphoprotein
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Gaps

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Length 206; Indels 180

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nef protein - human immunodeficiency virus type 1 (isolate LV)
N.Alternate names: 3'-orf protein; orf-F protein
C.Species: human immunodeficiency virus type 1, HIV-1
C.Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C.Accession: A04007
R.Muesing, M.A.: Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D. Mature 313, 450-458, 1985
A.Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy ret
A.Reference number: A93355; MUID:85111157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASLJ12

nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)

N;Alternate names: 3' orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo saptens (man)
C;Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: A04006

R;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. SG1. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune re
A;Reference number: A94093; MUID:86177573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-206 <ARY>
A;Cross-references: EMBL:M11840; NID:9328453; PIDN:AAA45001.1; PID:9328458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTGGY 229
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121 FPDXQNYTPGPGVRYPLTFGWCYKLVPVEPDKIEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Genetics:
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Pred. No. 6e-79;
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Pred. No. 2.1e-79;
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                                          290 LEWRFDSRLAFHHVARELHPEYFKNC 315
                                                              181 LEWRFDSRLAFHHVARELHPEYFKNC 206
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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A; Molecule type: DNA
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R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acquasterence number: S03244; MUID:86067228
                                                                                                                                                                        7
                                                                                                    C; Accession: $43467

R; Freudu, J; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.

Eur. J Biochem. 221, 811-819, 1994

A; Title: Stability and proteolytic domains of Nef protein from human immunodeficiency

A; Reference number: $43467; MUID: 94229079

A; Status: preliminary

A; Status: preliminary

A; Status: 1-205 cFRES

C; Superfamily: AIDS nef protein
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N'Alfernate names: 3'-orf protein
C'Species: human immunodeficiency virus type 1, HIV-1
C'Spacies: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
                    $43467
nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
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Pred. No. 1.7e-79;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                               Score 1115; DB 2;
Pred, No. 1.7e-79;
0; Mismatches 2;
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Best Local Similarity 99.0%;
Matches 203; Conservative
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Best Local Similarity 98.55
Matches 203; Conservative
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nef protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
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N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 31-Jan-1997
C;Accession: A04005
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A;Cross-references: EMBL:X03188; NID:g61556; PIDN:CAA26947.1; PID:g61557
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Pred. No. 5.2e-78;
                                                                                                             Score 1096; DB 2;
Pred. No. 5.2e-78;
1; Mismatches 3;
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; Mismatches
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96.6%;
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96.68;
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A,Residues: 1-206 <CAR>
A,Cross-references: EMBL:211530;
C,Superfamily: AIDS nef protein
                 C,Genetics:
A,Gene: nef; 3'-orf; orf-F
C,Superfamily: AIDS nef protein
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                                                                                                                                   Best Local Similarity 96.6
Matches 199; Conservative
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R; Carlini, F.
submitted to the EMBL Data L:
A; Reference number: S33979
A; Accession: S33986
A; Status: preliminary
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Matches 199;
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N.Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: S03445
R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa N.Vicle: Polymorphism of the 3' open reading frame of the virus associated with the acquance number: S03244; MUID:86067228
A;Mccession: S03245
A;Moclecule type: DMA
A;Residues: 1'206 <RAT>
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nef protein - Human immunodeficiency virus type 1, HIV-1

C;Species: Human immunodeficiency virus type 1, HIV-1

C;Species: Human immunodeficiency virus type 1, HIV-1

C;Species: Human immunodeficiency virus type 1, HIV-1

C;Accession: JC5400

C;Accession: JC5400

C;Accession: JC5400

R;Macreadie, T.G:; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.

Biochem: Biophys: Res. Commun. 232, 707-711, 1997 HIV-1 Nef N-terminal peptides to ye A;Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to ye A;Recission: JC5400; MUID:97271389

A;Recission: JC5400

A;Molecule type: protein

A;Residues: 1-206 <AAC>

C;Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activents.

C;Superfamily: AIDS nef protein

F;2-206/Product: nef protein #status predicted <AAT>
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                                     MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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Pred. No. 4.3e-78;
1; Mismatches 5;
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 4; Mismatches
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|larity 97.1%;
|Conservative
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virus ( Dandeka:

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A; Molecule type: DNA
A; Residues: 1-218 <ANN>
A; Residues: 1-218 <ANN>
Cross-references: GB: MND: g326426; PIDN: AAA44222.1; PID: g326431
R; Steuler, H.; Storch Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A; Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as det.
A; Reference number: S21990
A; Accession: S21993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L.; Louie, A.; Gallo, R.C.; Streicher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X61358; NID:g60177; PIDN:CAA43629.1; PID:g584027; EMBL:X613 A;Accession: S21995
A;Molecule type: DNA
A;Residues: 1-7 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43623.1; PID:g584028; EMBL:X613
A;Accession: S21997
                                                                                  nef protein - human immunodeficiency virus type 1 (isolate BR)
N'Alternet names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Oate: al-Dec-1989 isolates is desquence_revision 31-Dec-1989 itext_change 16-Jul-1999
C;Accession: D31667; S21993; S21997; S21999; S21991
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; I
Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency values in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state
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October 12 S25937

C.Species: human immunodeficiency virus type 1

C.Species: human immunodeficiency virus type 1, HIV-1

C.Species: human immunodeficiency virus type 1, HIV-1

C.Species: D.SEP-1994 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999

C.Species: S2-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999

R.Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; S

Nature 349, 745-746, 1991

A.Title: Sequence analysis of original HIV-1.
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A;Accession: S21999
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; Pred. No. 5.5e-72;
12; Mismatches 7;
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%;
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R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dord
nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nef protein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1,

C;Accession: $24985

R;Harris, M.; Hislop, S.; Patsilinacos, P.; Neil, J.C.

Submitted to the EMBL Data Library, November 1991

A;Reference number: $24985

A;Reference number: $24985

A;Accession: $24985
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A;Cross-references: EMBL:X63044; NID:g60123; PIDN:CAA44770.1; PID:g60124
C;Superfamily: AIDS nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLTYSQKRQDILDLWIYHTQGY
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                                                                                                                                 A.Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A.Reference number: A93353; MUD:85111123
A.Rocession: A04005
A.Rocession: A04005
A.Residues: 1-205 <RAT>
C.Genetics:
A.Generics:
A.Generics:
C.Genetics:
A.Generics:
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Pred. No. 6.9e-77;
4; Mismatches 3;
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Best Local Similarity 96.1%;
Matches 198; Conservative 4
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nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)
N.Alternate names: 3'-orf protein
C.Specides: human immunodeficiency virus type 1, HIV-1
C.Specides: human immunodeficiency virus type 1, HIV-1
C.Specides: b. Josephs, virus type 1, HIV-1
C.Specides: b. Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett R.Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett Nucleic Acids Res. 13, 8219-8229, 1985
A.Title: Polymorphism of the 3' open reading frame of the virus associated with the a A.Reference number: S03244; MUID:86067228
A.Molecule type: mRNA
A.Molecule: 1-182 - KRAT>
A.Residues: 1-182 - KRAT>
A.Cross-references: EMBL:X03189; NID:961552; PIDN:CAA26948.1; PID:91335562
                                                                                                                                                                                                     C; Accession: I44001
R; Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A; Title: Complete nucleotide sequence, genome organization, and biological propertit.
A; Reference number: A44001; MuID: 93021387
A; Accession: I44001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 MGGKWSKSSVVGWPTVR-----ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 PAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 214;
                                                                                                                                                          A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 182;
                                                                                    nef protein - human immunodeficiency virus type 1 (strain YU-2)
N/Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.0%; Score 991.5; DB 1;
ilarity 84.2%; Pred. No. 7.5e-70;
Conservative 12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 987; DB 2;
Pred. No. 1.4e-69;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: nef; 3'-orf; orf-F
C; Superfamily: AIDS nef protein
C; Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.8%;
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C,Superfamily: AIDS nef protein
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                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-214 <LIY>
A; Cross-references: GB:M93258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 179; Conserv
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Best Local Simi
Matches 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nef protein - human immunodeficiency virus type 1 (isolate ARV-2)

N.Alternate names: 3'-orf protein; orf-F protein
C;Species: and order core protein; orf-F protein
C;Species: and order capiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A04009
R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A; Accession: A04009
A;Accession: A04009
A;Accession: A04009
A;Accession: A04009
A;Cross-references: GB:K02007; NID:g328658; PIDN:AAB59883.1; PID:g328667
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
                                                                                                                                                          1991
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A;Reference number: $25937; MUID:91156044
A;Accession: $25937
A;Accession: $25937
A;Accession: $25937
A;Accession: $25937
A;Accession: $25937
A;Relequie type: nucleic acid sequence not shown; translation not shown A;Melequie type: nucleic acid
A;Residues: 1-206 <GUO>
A;Residues: 1-206 <GUO>
A;Residues: 1-206 <GUO>
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, March
C;Superfamily: AIDS nef protein
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                                                                                                                                                                                                                                                                                                                                                 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                                                                                                                                                                                  ; Score 1007; DB 2; Length 206;
; Pred. No. 4.4e-71;
18; Mismatches 11; Indels
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85.2%; Pred. No. 2.7e-70;
tive 16; Mismatches 11;
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                                                                                                                                                                                                                                                    44.7%;
85.9%;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.99
Matches 177; Conservative
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Best Local Similarity 85.2
Matches 179; Conservative
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N:Alternate names: 3'-orf protein: Orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 YEPDWQNYTPGPGVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 IFPDWONYTPGPGIRYPLIFGWCFQLVPVDPQEVEEATEREDNCLLHPMCQQGMEDPERQ 180
                                                                                                                                                                                                                                          165 AWLEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI 223
                                                                                                                                                                                                                                                                      110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                              Gaps
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD
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                                             Length 212
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nef protein - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: 3' orf protein; orf F protein
C;Species: human immunodeficiency virus type 1, HIV-1
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                                                                                              Indels
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                                                                                              19;
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                                             ; Score 911; DB 1;
; Pred. No. 1.4e-63;
23; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                         289 VLEWRFDSRLAFHHVARELHPEYFKNC 315
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Keywords: AIDS; immunodeficiency
                                           40.48;
                                                                                              Conservative
                                                                       Similarity
                                                                                              Matches 164;
                                                Query Match
Best Local
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C;Superfamil
C;Keywords:
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N:Alternate names: 3'-orf protein; orfF protein
C;Species: human immunodeficiency virus Zr-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C;Accession: F26192
C;Accession: F26192
C;Accession: F26192
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotin
A;Reference number: A26192; MUID:87248097
A;Accession: F26192
A;Molecule type: DNA
A;Residues: 1-212 <SRI>A;Reference C; GB:K03458; GB:M16322; NID:9329398; PIDN:AAA45381.1; PID:9329404
                                                                                                                                                                                                                                                                                                                                nef protein (clone HAT3) - human immunodeficiency virus type 1

N.Alternate names: 3'-orf protein

N.Alternate names: 3'-orf protein

S.Species: human immunodeficiency virus type 1, HIV-1

C.Species: 13-874

C.Species: N.S.Species: N.S.Species: N.S.Species: N.S.Species: N.S.Species: N.S.Species: N.S.Species: N.S.Species: N.Species: N.Speci
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%; Score 987; DB 2; Length 204; 84.5%; Pred. No. 1.6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Gene. nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.8
Best Local Similarity 84.5
Matches 174; Conservative
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|NC 182
                                                                                                                                                                     314 NC 315
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Nalternate names: 3'-orf protein. orf-F protein

Nalternate names: 3'-orf protein. orf-F protein

C; Species: simian immunodeficiency virus SIVopz

A; Note: host Pan troglodytes (chimpanzee)

C; Date: 30. Sep-1991 *sequence_revision 30. Sep-1991 *text_change 16-Jul-1999

C; Accession: S09991

N; Huet, T: Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 356, 359, 1990

A; Reference number: S09983; MUD:90259077

A; Reference number: S09983; MUD:90259077

A; Status: nucleic acid sequence not shown; translation not shown

A; Mealduse: 1-205 < HUE>

A; Residues: 1-205 < HUE>

A; Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36408.1; PID:958877

C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae N'Alternate names: IgD-binding protein; protein D C; Species: Haemophilus influenzae A; Variety: strain 3639 C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 C; Accession: S59931: S47333 R; Song, X.M.; Forsgren, A. Janson, H. Infect. Immun. 63, 696-699, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:235656; NID:9525213; PIDN:CAA84715.1; PID:9525214 A;Experimental source: strain 3639 C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 25.7%; Score 578.5; DB 2; Length 364; Best Local Similarity 47.1%; Pred. No. 2.1e-37; Matches 145; Conservative 19; Mismatches 71; Indels 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: The gene encoding protein D (hpd) is highly A,Reference number: $59931; MUID:95122210
A,Accession: $59931
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 832; DB 1;
Pred. No. 1.9e-57;
7; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 LEWRFDSRLAFHHVARELHPEYFKN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Sc
Similarity 70.2%; Pr
44; Conservative 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: AIDS nef protein
Keywords: AIDS; immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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Best Local Simi
Matches 144;
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C;Accession: B44963
R:Stnivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, AIDS Res. Hum. Retroviruses S. 121-129, 1989
A:Title: Mclecular characterization of HIV-1 isolated from a serum collected in 1976: r A;Reference number: A44963; MuID:89228766
A:Accession: B44963
A:Accession: B44963
A:Accession: B44963
A:Residues: 1-205 <SRI>
A;Residues: 1-205 <SRI>
A;Coss.references: GB:M15896; NID:g329392; PIDN:AAB53951.1; PID:g329397
A;Cross-references: GB:M15696; NID:g329392; PIDN:AAB53951.1; PID:g329397
C;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; Immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nef protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1,
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01673
FABIZON: M.; Wadn-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of 1
A;Reference number: 214389; MUID:86245056
A;Reference number: 214389; MUID:86245056
A;Accession: T01673
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-209 <ALI>A;Residues: 1-209 <ALI>A;Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28017.1; PID:g60235
C;Superfamily: AIDS nef protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOGYFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVG----AASRDLEKHGAITSSNTAATNAAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 224
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                                                                                                                                                                                                                                                                                                                                                       Length 205;
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                                                                                                                                                                                                                                                                                                                                                       ; Score 837; DB 1;
; Pred. No. 7.6e-58;
23; Mismatches 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.0%; Score 834.5; DB 2
70.1%; Pred. No. 1.2e-57;
1ve 26; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                       37.1%;
73.2%;
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Best Local Similarity 73.23
Matches 153; Conservative
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Best Local Similarity
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Haemophilus infl

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Glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor - Haemophilus influe N.Alternate names: immunoglobulin D-binding protein; protein D C.Species: Haemophilus influenzae A:Variety: strain Eagan: strain HK695 C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 C.Accession: S59934; S59935; S47336; S47337 F.Song, X.M.; Forsgren, A.; Janson, H. Infect. Immun. 63, 696-699, 1995 A.Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus inf A.Reference number: S59931; MUID:95122210
                                                                                                                                                                        R;Janson, H.; Heden, L.O.; Grubb, A.; Ruan, M.; Forsgren, A.
Infect. Immun. 59, 119-125, 1991
A;Title: Protein D, an immunoglobulin D-binding protein of Haemophilus influenzae: c
A;Reference number: A43576; MUID:91099948
A;Accession: A43576
                           - Haemophilus influe
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                                                                                                                                                                                                                                                                                                                       A Molecule type: DNA
A,Residues: 1-364 - CANN
A,Residues: 1-364 - CANN
A,CTOSS-references: GB-M37487; NID:9148970; PIDN:AAA24998.1; PID:9148971
A,Experimental source: isolate 772
C,Reywords: Ilpoprotelair, Phosphoric diester hydrolase; surface antigen
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-364/Product: 91ycerophosphodiester phosphodiesterase #status predicted
glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor - Haemophili. N.Alternate names: immunoglobulin D-binding protein; protein D. A.Yariety: Haemophilus influenzae A.Yariety: isolate 772 C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999 C; Accession: A43576
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A.Residues: 1-364 - SOW>
A.Cross-references: EMBL:Z135660; NID:g525221; PIDN:CAA84719.1; PID:g525222
A.Experimental source: strain HK695
C.Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
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A:Accession: S59935
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A; Residues: 1-364 <SON>
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Best Local Simmatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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Risong, X.M.; Forsgren, A.; Janson, H.
Infect. Immun. 63, 696-699, 1995
A;Title: The gene encoding protein D (hpd) is highly conserved among Haemop A;Reference number: S59931; MuID:95122210
A;Reference number: S59932
A;Rolecule type: DNA
A;Residues: 1-364 <SON>
A;Residues: 1-364 <SON>
A;Cross references: EMBL:235657; NID:9525215; PIDN:CAA84716.1; PID:9525216
A;Experimental source: strain 3640
C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
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                                                                                  139 RFPLWKSHFRIHTFEDEIEFIQGLEKSTGKKVGIYPEIKAPWFHHQNGKDIAAETLKVLK 198
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                                                                                                                                                                                                                                                                                                                                                                            GLIHSQRRQDILDLWIYHTQGYFPDWQ------NYTPGFGVRYPLTFGWCYKLVPV 257
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  CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL 78
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                                                         61 VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGK--
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Best Local Similarity 47.1%; Pred. No. 2.1e-37;
Matches 145; Conservative 19; Mismatches 71
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RESULT

QY         208 GLIHSQRRQDILDLMIYHTQQYFPDWQNYTPQPGVRYPLTFGWCYKLVPV           Db         247ETQEKDSKGYWYNYNYDHMFKPGAMAEVVKYADGVGPGW-YMLVNK 29.           QY         258 EPDKV 262           I         I           Db         292 EESKPDNI 299	RESULT 27 G64066 g1ycercophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (stra. N; Alternate names: IgD-binding protein; protein D C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae C:Species: Haemophilus influenzae R.C.; Spacession: G64086 R:Fleischmann, R.D.; Annie, W.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage C:Accession: G64086 A; Scotta. Mole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Accession: G64086 A; Accession: G64086 A; Accession: G44086 A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-364 <tigr> A; Coss. references: GB:U32751; GB:L42023; NID:g3212200; PIDN:AAC22348.1; PID:g1573690 A; Experimental source: strain Rd KW20 C; Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen</tigr>	Query Match  24.9%; Score 562.5; DB 2; Length 364;  Best Local Similarity 46.1%; Pred. No. 3.7e-36;  Matches 142; Conservative 21; Mismatches 72; Indels 73; Gaps 11;  Qy 1 CSSHSSNMANTOMKSDKIITAHRGASCYLEHTLESKALAFAQQADVLEQDLAMTKOGRL 60   1	Qy 208 GLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGFCVRYPLTFGWCYKLVPV 257
F:1-18/Domain: signal sequence #status predicted <sig> F:19-364/Product: protein D #status predicted <mat> Ouery Match Best Local Similarity 47.1%; Pred. No. 2.1e-37; Matches 145; Conservative 19; Mismatches 71; Indels 73; Gaps 11;</mat></sig>	0y 1 CSSHSSNMANTOMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAWTKDGRL 60	RESULT 26 S5993 glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strain 6 N; Alternate names: Immunoglobulin D-binding protein; protein D C; Specs: Haemophilus influenzae A; Variety: strain 6-7626 C; Specs: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 C; Accession: S5993; S47335 R; Song, X.M.; Forsgren, A.; Janson, H. Rifect. Immun. 63, 696-699, 1995 A; Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus influen A; Reference number: S5993; MUD:9512210 A; Accession: S59933 A; Accession: S59933 A; Accession: S59933 A; Reference number: S59931; MUD:9512210 A; Accession: S59933 A; Accession: S5993	Query Match         25.4%;         Score 572.5;         DB 2;         Length 364;           Best Local Similarity 46.8%;         Pred. No. 6.1e-37;         Accal Similarity 46.8%;         Pred. No. 6.1e-37;           Matches 144;         Conservative 19;         Mismatches 72;         Indels 73;         Gaps 11;           QY         1 CSSHSSNMANTOMKSDKIIIAHRGASGYLPHTLESKALAFAQOADYLEQDLAMTKDGRL 60           DD         19 CSSHSSNMAKTQMKSDKIIIAHRGASGYLPHTLESKALAFAQQADYLEQDLAMTKDGRL 78           QY         61 VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETROGGR

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trans-activating transcription regulator - human immunodeficiency virus type 1 (isol
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                            RiArya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity
A;Reference number: A94093; MUID:86177573
A;Accession: A04017
                                                                                                                                                                                                                                   A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
C:Accession: A04017
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C; Superfamily: AIDS trans-activating transcription regulator
C; Keywords: AIDS; immunodeficiency; transcription regulation
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Pred. No. 2.7e-30;
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98.8%; Pred. No. ....
0; Mismatches
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378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
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Matches 84; Conserv
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A; Residues: 1-95 <ARY>
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A; Residues: 1-86 CCAR>

A; Residues: 1-86 CCAR>

A; Cross-references: EMBL:211530; NID:960192; PIDN:CAA77625.1; PID:960196

R; Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Brfle, H.; Sumner-Sm

Nucleic Acids Res. 20, 5311-5320, 1992

A; Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c

A; Reference number: S26385; MUID:93065196
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                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 VVIHDHFLDGLTDVAKKFPHHHRKDGRYYVIDFTLKEIQSLEMTENFETKDGKQAQVYPN 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 KYGYDKKTD-----MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK---- 246
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A;Accession: S59936
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-344 <SON>
A;Cross-references: EMBL:235661; NID:9525223; PIDN:CAA84720.1; PID:9525224
A;Experimental source: strain NCTC 8468
C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SKSSVVG-WPTVRERMRRAEPAADGVGAASRDLE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GLIHSQRRQDILDLWIYHTQGYFPDWQ------NYTPGFGVRYPLTFGWCYKLVPV 257
                                                                                                                                                                                                                                                                                                                                                                                                                   61 VVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGK----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ----ETQEKDPKGYWV----NYNYDWMFKPGAMAEVVKYADGVGP-----GW-YMLVNK 291
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                                                                                                                                                                                                                                                                                                                  1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL 60
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1991 A; Reference number: S33979 A; Accession: S33982
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C, Superfamily: AIDS trans-activati
C, Keywords: AIDS; immunodeficiency
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A; Residues: 1-86 <SID>
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Best Local Similarity
Matches 85; Conserv
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P04614 P20893

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' or fencedes a phosphorylated GTP-binding protein resembling
an oncogene product.";
Nature 330:266-269(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (BRU isolate) (HIV-1), and
human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
Viruses; Retroid viruses; Retroidiate; Lentivirus.
NCBI_TaxID=11686, 11698;
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SEQUENCE FROM N.A. (CLONE PNL4-3).
STRAIN-ISOLATE NEW YORK-5;
Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.,
Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.; "Nucleotide sequence of the AIDS virus, LAV."; Cell 40:9-17(1985).
                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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                                                                                                                                                                                                                                                                              206 AA
NEF_HV2KR
TAT_HV1SC
TAT_HV1S1
TAT_HV1S1
TAT_HV1Y2
TAT_HV1Y2
TAT_HV1Y2
NEF_SIVS4
NEF_SIVS4
NEF_SIVS9
                                                                                                                                            TAT_HV1A2
TAT_HV1OY
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MEDLINE-85099333; PubMed-2981635;
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NEF_HV1BL 1

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DT 16-OCI

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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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NEF_HV1B1
GLPQ_HAEIN
TAT_HV1B1
TAT_HV1PV
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Maximum Match 100%
Listing first 45 summaries
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NEF_HV1EL
NEF_HV1Z6
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NEF_HV1MN
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NEF_SIVC2
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NEF_HV1SC
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TAT_HV1BR

    protein search, using sw model

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length: 2000000000
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"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                            61 QEEEEVGFPVTPQVPLRPMTYKAANDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTGGY 120
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                             230 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; PubMed-3118220;
GUY B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky
                Interpro: IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.
                                                                                                                                                        DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
                                                                                                                                                                               Indels
                                                                           V -> I (IN CLONE PNL4-3).
T -> A (IN CLONE PNL4-3).
A -> V (IN CLONE PNL4-3).
T -> N (IN CLONE PNL4-3).
77453FC80B6004F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                 PHOSPHORYLATION (BY PKC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11700;
                                                                                                                                                                               ö
                                                                                                                                                       Score 1130; DB 1;
Pred. No. 1e-86;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA.
                                                                                                                                                                                                                                                                                                                                         290 LEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS/lymphadenopathy retrovirus.";
Nature 313:450-458(1985).
                                                                                                                                                50.1%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85111157; Pubmed-2982104
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33
51
23342
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                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
KO2013; NEF$BRU
M19921; NEF$NL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oncogene product
                                                                                                                                                                   Similarity
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51
206 l
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NEF_HVIPV
ID NEF_HVIPV
P03405;
                                                                                                                                                                             Matches 206;
                                                                                                                                                         Query Match
                                                                                                                        SEQUENCE
                                                                 MOD_RES
                                                                                       VARIANT
VARIANT
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                                                                                                              VARIANT
                               Pfam;
AIDS;
                                                       LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY.
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-!- FUNCTION: NEF HAS GIPASE, GTP-BINDING AND AUTOPHOSPHORYLATING AUTOPHOSE, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QEEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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MEDILINE-9733745; Pubmed-9194185;
Grzeslek S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,
Tjandra N., Wingfield P.T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                       MYRISTATE.
EDE64281A17C6735 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                          Score 1114; DB 1;
Pred. No. 2.1e-85;
3; Mismatches 2;
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                             -; NOT_ANNOTATED_CDS
                                                       PIR; A04007; ASLJVL.
HSSP; P03406; IEFN.
HIV; K02083; NEF$PV22.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; I.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                 206 AA; 23352 MW;
                                                                                                                                                                                                                                                                                                                                                                             49.4%;
ilarity 97.6%;
Conservative
EMBL; K02083; AAB59874.1;
EMBL; X01762; -; NOT_ANNOT
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                    170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                                                                                        61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY 120
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MEDLINE-86177573; Pubmed-3008154;
Arya S.K., Gallo R.C.;
"Three novel genes of human T-lymphotropic virus type III: immune reactivity of their products with sera from acquired immune deficiency syndrome patients.";
                                                                                                                                                                                                               110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                  1 MGGKWSKSSVIGWPTVRERMRRAEPAADGVGAASQDLEKHGAITSSNTAATNADCAWLEA
                                                                                                                                                                                                                                                                                                                                                           230 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                              ö
                                                                                                                                         Length 206,
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (clone 12) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11679;
                                                                    MYRISTATE.
ED81F68F6B61278E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Created)
13-Add-1987 (Rel. 05, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Scl. U.S.A. 83:2209-2213(1986).
                                                                                                                                     Score 1111; DB 1;
Pred. No. 3.8e-85;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION
                             Pfam; PF00469; F-protein; 1,
AIDS; Myristate; GTP-binding; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             290 LEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LEWRFDSRLAFHHVARELHPEYFKNC 206
07-JUL-97.
IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001558; F-protein
                                                                                     23414 MW;
                                                                                                                                         Query Match
Best Local Similarity 97.1%;
Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an oncogene product.";
Nature 330:266-269(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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HSSP; P03406; 1EFN.
HIV; M11840; NEF$PCV12.
                                                                                     206 AA;
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P04324:
                  InterPro;
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NEF_HV112
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                                                                                                                                                                        110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                           an oncogene product.";
Nature 330:266-269(1987).
-i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-i- FUNCTION: NEF HAS GTPASE, T SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                              1 MGGKWSKSSVVGWPAVRERMRRAEPAADGVGAASRDLEKHGAITSSVTAANNAACAWLEA
                                                                                                                                                                                                                                                            QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                        ;
0
                                                                                                      Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HIV-1).
                                                                                                                                        Indels
                                  MYRISTATE,
218F5B2980F79A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (BH8 isolate) (Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
                                                                                                    49.1%; Score 1108; DB 1;
97.1%; Pred. No. 6.7e-85;
tive 4; Mismatches 2
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HSSP; P03406; 1EFN.
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Pfam; PF00469; F-protein; 1.
                                                206 AA; 23366 MW;
PF00469; F-protein; 1. Myristate; GTP-binding.
                                                                                                                                        Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                      Similarity
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NCBI_TaxID=11684;
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P05855;
                                                  SEQUENCE
                                                                                                      Query Match
                                                                                                                         Local
                   AIDS;
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Matches 185;
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P19545;
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                                                                                                                      110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                       229
                                                                                                                                                                                                                       230 FPDWQNYTPGPGVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
                                                                                                                                                                                                                                     Gaps
                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIVELLAGY 168:79-89(1989).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-!- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS
HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
                                                                                                                                   170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                  1;
                                                                 Query Match

48.3%; Score 1088.5; DB 1; Length 205;
Best Local Similarity 96.6%; Pred. No. 2.8e-83;
Matches 199; Conservative 3; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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218 AA; 25032 MW; FC4DAEA1045C460E CRC64;
                  MYRISTATE.
BEC12F6650DDD111 CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                                  218 AA.
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                                                                                                                                                                                                                                                                                      180 LEWRFDSRLAFHHMARELHPEYFKNC 205
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                              205 AA; 23305 MW;
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AIDS; Myristate; GTP-binding.
LIPID
AIDS; Myristate; GTP-binding.
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HIV; M21098; NEFSBRVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11693;
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P12479;
                              SEQUENCE
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Length 218;

Score 1019; DB 1; Pred. No. 1.8e-77;

45.2%; 84.1%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                 QDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLH 275
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                                                       MGGKWSKSSVVGWPTVRERMR------RAEPAADGVGAASRDLEKHGAITSS 155
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MEDLINE-90317906; PubMed-2370688;
MEDLINE-90317906; PubMed-2370688;
MEDLINE-90317906; Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
"Human immunodeficiency virus type 1 cellular host range,
replication, and cytopathicity are linked to the envelope region of
the viral genome.";
J. virol. 64:4016-4020(1990)
J. virol. MEG-400-4020(1990)
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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  16;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11690;
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86.4%; Pred. No. 2.1e-76;
tive 19; Mismatches 8; Indels
7; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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  Mismatches
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  12;
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Best Local Similarity 86.49
Matches 178; Conservative
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Montagnier L., Lecocq J.-P.;
"HIV F.7" orf encodes a phosphorylated GTP-binding protein resembling an oncogene product." and product and product and an oncogene product." Nature 330:266-269(1987).
-! FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-85090453; PubMed-2578227; MEDLINE-85090453; PubMed-2578227; Steiner K.S., Steiner K.S., Stemplen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A., Levy J.A., Dina D., Luciw P.A.; "Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH
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                                                                                                                                                                                                                                                                                                                                                                                                                             POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; PubMed-3118220;
GUY B., Kleny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                Human immunodeficiency virus type l (ARV2/SF2 isolate) (HIV-l).
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11685;
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                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
           210 AA
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LIPID 2
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Science 227:484-492(1985).
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        STANDARD;
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      NEF_HV1A2
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NEF_HV1RH
ID NEF_HV
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110 MGGKWSKSSVVGWPTVRERMRRA----EPAADGVGAASRDLEKHGAITSSNTAATNAAC 164
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MEDLINE=90148544; PubMed=2559749;
Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S. Hatt T., Dazza H.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S. A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: NEF HÁS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-i- MISCELLANEDUS: THE OXI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11699;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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                                                                                                                                                                                                             211 AA
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                                                             290 LEWRFDSRLAFHHVARELHPEYFKNC
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Pfam; PF00469; F-protein; 1
AIDS; Myristate; GTP-binding.
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P20886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QEDEDEEVGFPVRPQVPLRPMTFXAAVDLSHFLKEKGGLDGLVFSQKRQDILDLMVYHTQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GYFPDWQNYTPGPGTRYPLTFGWCFKLVPVEPDKVEEATEGENNSLLHPICLHGMDDPEK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 Q -- EEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER
                                                                                                                                                                                       FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                      (RF/HAT isolate) (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                          Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           MYRISTATE (BY SIMILARITY).
8F836FE8980F084C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                              Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                 Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.1%; Score 994; DB 1;
84.6%; Pred. No. 2e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEF_HVIY2 STANDARD; PRT; 214 AA. P35959; 01-JUN-1994 (Rel. 29, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
         01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
44.1%; Score 994; DB
Best Local Similarity 84.6%; Pred. No. 2e-7;
Matches 176; Conservative 16; Mismatches
                                                                                                                                                                             Submitted (XXX-1987) to the HIV data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 EVLEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 EVLVWKFDSRLAFHHVAREKHPEYYKDC 208
                                                                       Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-93021387; PubMed-1404605;
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                       208 AA; 23532 MW;
                                                                                                                                                                                                                                                                                                                               EMBL; M17451; AAA45058.1; -. HSSP; P03406; 1EFN.
                                                                                                                                                                                                                                                                                                                                                          HIV; M17451; NEFSRF.
                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=36377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 MGGKWSKSSVVGWPTVR-----ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLWIYHTOGYFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 219
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                                           in vivo: evidence
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Submitted (DEC-1988) to the HIV data bank.
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
          and biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidenc for limited defectiveness and complementation.";
J. virol. 66:6587-6600(1992).
-1- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 991.5; DB 1; Length 214;
; Pred. No. 3.3e-75;
12; Mismatches 11; Indels 11.
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Viruses; Retroid viruses; Retroviridae; Lentlvirus.
NCBL_TaxID=11688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE (BY SIMILARITY).
E188D43D7B084D04 CRC64;
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Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 HGMDDPEREGLEWRFDSRLAFHHVARELHPEYYKN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKN 314
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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HSSP; P03406; 1EFN.
InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24532 MW;
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84.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00469; F-protein;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90347835; PubMed-2284920; Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.; Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.; Trail determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation."; J. Virol. 64:4390-4338(1990).
-i. FUNCTION: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                           43.5%; Score 981; DB 1; Length 216; 81.9%; Pred. No. 2.5e-74; ive 15; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYRISTATE (BY SIMILARITY)
A0B1007D14E46E32 CRC64;
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D163FFA8C71529DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P19546;
P19546;
01-FEB-1991 (Rel. 17, Created)
1-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 315
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                     HIV; M38429; NEFSJRCSF.
InterPro; IPROUSSS8; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
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                                                                                                                                                                                                                                               216 AA; 24567 MW;
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                             EMBL; M38429; AAB03750.1;
HSSP; P03406; 1EFN.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.99
Matches 177; Conservative
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NEF-HV1S1

DC 01-FEB

DT 01-FEB

DT 01-FEB

DT 01-FEB

DT 01-FEB

DT 01-FEB

DT 01-FEB

DT 01-FEB

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OS V1ruse

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CC 1-FE

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MEDLINE-88039140; Pubmed-3118320;
GUY B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
an oncogene product.";
Nature 330:266-269(1987).
                                                         MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 166
                                                                                                                                   QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPE 286
                                                                                                                                                                                               LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT 226
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                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-86245056; PubMed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
Cell 46:63-74(1986).
                                                                           -!- FUNCTION: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
   9e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%; Score 927.5; DB 1;
79.1%; Pred. No. 6.4e-70;
tive 24; Mismatches 18;
              Pred. No. 9e-74; Mismatches
                                                                                                                                                                                                                                                                                                                                                    206 AA
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84.28; Fit. 16; 1
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
LIPID 2 2 MYF
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            Similarity 84.29
76; Conservative
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                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Best Local Similarity
Matches 163; Conserv
              Best Local Sim
Matches 176;
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P04604;
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NEF_HV1EL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
Gene 52:71-82(1987).
                                                                                                                                                                                                                  protein resembling
                                                                                          228
                                                                                                                     229 YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERE 288
MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                             9
                           MEDLINE-88039140; PubMed-3118220;
Guy B., Kleny M.-P., Riviere Y., le Peuch C., Dott K., Girard M., Montagnier L., Lecocq J.-P.;
HITY F/3' orf encodes a phosphorylated GTP-binding protein resemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an oncogene product.";
Nature 330:266-269(1887).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-- ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                            170 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Srinivasan A., Anand R., York D., Ranganathan P., Feorino
Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
Sanchez-Pescador R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYRISTATE.
; EC095A1B263047CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA.
                                                                                                                                                                                                                                                                                289 VLEWRFDSRLAFHHVARELHPEYFKN 314
||:|||:||||| ||:|||:||
181 VLKWRFNSRLAFEHKAREMHPEFYKN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87248097; Pubmed-303660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K03458; AAA45381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P03406; IEFN.
HIV; K03458; NEF$26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEF_HV1Z6
P04602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- FUNCTION: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLAIING ACTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN.
-I- MISCELLANDOUS: NDK, ISOLATED FROM A ZATRIAN PATIENT AFFECTED WITH AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QEESEEVGFPVRPQVPLRPMTYKEAVDLSHFLKEKGGLEGLIHSKKRQEILDLWYVTQG 120
                                                                                                          223
                                                                                                                                             MEDLINE-90034200; PubMed-2806917;
Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
Hampe A., Chermann J.C.;
                                                                                                                                                                                                                       YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
110 MGGKWSKSSVVGWPTVRERM-----RRAEPAADGVGAASRDLEKHGAITSSNTAATNAAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
Gene 81:275-284 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGGRWSKSSIVGWPAIRERIRRTDPRRTDPAADGVGAASRDLEKHGAITSSNTRDTNADC
                                                                                                             AWLEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE (BY SIMILARITY).
09036C2F81D45D5E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 AA
                                                                                                                                                                                                                                                                                                                                                                 284 DPEREVLEWRFDSRLAFHHVARELHPEYFKNC 315
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Best Local Similarity 77.3%
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEF_HV1ND
P18801;
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Gaps

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Indels

19;

Query Match
40.4%; Score 911; DB 1;
Best Local Similarity 77.4%; Pred. No. 1.6e-68;
Matches 164; Conservative 23; Mismatches 19.

Length 212;

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181

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 MGGKWSKSSVVGWPTVRERMRRAEP---AADGVGAASRDLEKHGAITSSNTAATNAACAW 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                         Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collaiti E., Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jf.;

"Enrelope sequences of two new United States HIV-1 isolates.";

Virology 164:531-536(1988).

-!- FUNCTION: NEF HAS GTPASE, GTP-EINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEREN TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

-!- MISCELLANBOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 842; DB 1; Length 18
Pred. No. 6.8e-63;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRISTATE (BY SIMILARITY)
2C5B5A6E3EF13B26 CRC64;
                                        01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
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01-NOV-1988 (Rel. 09, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kba protein) (3'ORF)
        182 AA.
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MEDLINE-88219542; Pubmed-3369091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89228766; PubMed-2713163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; MI7449; NEF$MN.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
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llarity 87.4%;
Conservative 11
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HSSP; P03406; 1EFN.
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        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     PATIENT IN 1984.
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P05859;
      NEF_HVIMN
PO5856;
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OS Human

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YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERE 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.
Carswell J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYRISTATE (BY SIMILARITY)
869AB03E6E7893C4 CRC64;
                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negalive factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                                                            Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11703;
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                                                                                                                                                                                                                    205 AA.
                                                                           289 VLEWRFDSRLAFHHVARELHPEYFKNC 315
                                                                                                  181 LMWKFDSTLALKHRAYELHPEFYKD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-91090981; PubMed-2265025;
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                                                                                                                                                                                                                NEF_HV1U4
P24741;
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(HIV-1)

Local

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Gaps

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Length 182;

Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr'R., Getchell

RESULT 18 NEF\_HV1MN

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                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 166
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McCormick J., Ou C.Y., Myers G., Smith T., Chen E.; "MoLecular characterization of HIV-1 isolated from a serum collected in 1976: nuclectide sequence comparison to recent isolates and generation of hybrid HIV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOGY FPDWQNY TPGPGVRY PLIFGWCYKLV PVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                                                    AIDS Res. Hum. Retroviruses 5:121-129(1989).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence
of two isolates from African patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (MAL isolate) (HIV-1). Wrutuses: Retroid viruses; Retroviridae; Lentivirus.
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EA55B18AF412A9D0 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.1%; Score 837; DB 1; 73.2%; Pred. No. 2.1e-62; iive 23; Mismatches 25
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                                                                                                                                                                                                                                                                                                                                                                                 PIR; B44963; B44963.
HSSP, P01406; 1EFN.
Interpro: IPR001558; F-protein.
Pfam; PF00469; F-protein.
AIDS; Myristate; GTP-binding.
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                                                                                                                                                                                                                                                                                                                                                              EMBL; M15896; AAB53951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 153; Conservative
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P04603;
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 345:356-359(1990)
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD
an oncogene product.";
Nature 330:266-269(1987)
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
--- ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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Viruses; Retrold viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 834.5; DB 1;
; Pred. No. 3.4e-62;
26; Mismatches 30;
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70.1%;
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Best Local Similarity 70.1%
Matches 148; Conservative
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01-AUG-1990 (
16-OCT-2001 (
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P17664;
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Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,

"Enrelpe Stall F., Gallo R.C., Reitz M.S. Jr.;

"Envelope sequences of two new United States HIV-1 isolates.";

Virology 164:531-536(1988).

-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING

ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

-!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN

1984 IN SOUTHERN CALIFORNIA.
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                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus. VCBL_TaxID-11702;
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21E0A3EC99F1811F CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                HIV; X52154; NEFSCP2.
InterPro; IPRO01558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
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                                                                                                                                                                                           205 AA; 23850 MW;
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                 EMBL, X52154; CAA36408.1;
PIR; S09991; ASLJIK.
HSSP; P03406; 1EFN.
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.2'
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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P05857;
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NEF_HY1SC

ID NEF_HY1SC

DT 01-NOV

DT 16-070

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                                                                ;;
                                                                                                                                                                                                                                                                             61 QEEEEVGFPVRPQVPLRPMTYKAAVDLSHFLKEQGGLEGLI--TPREDKISLICGSTTHK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; Pubmed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecorg J.-P.;
"HIV F/3' or encodes a phosphorylated GTP-binding protein resembling an oncogene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING AGTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN.
-i- MISCELLANEOUS: IN THIS ISOLATE A WUTATION IN POSITION 124 ADDS A STOP CODON AND THE PROTEIN IS WUCH SHORTER THAN IN OTHER ISOLATES.
                                                                                                                                                                                                                                                QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                                                                                                                                                                                           110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                          230 FPDWQNYT--PGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-87299196; PubMed-3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallo R.C., Wong-Staal F., "Complete nucleotide sequences of functional clones of the AIDS
                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R. -S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11706;
   Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou Gallo R.C., Wong-Staal F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEF_HV1H2 STANDARD; PRT; 123 AA.
P04601; 009780;
13-Adc-1987 (Rel. 05, Created)
15-JUL-1997 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
; DB 1;
7.8e-61;
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIDS Res. Hum. Retroviruses 3:57-69(1987)
36.3%; Score 819; 75.5%; Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K03455; AAB50263.1; -. EMBL; AF033819; AAC82597.1; -HSSP; Q70627; 2NEF.
                                                             Conservative
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (210 AA).
                                Best Local Sim
Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS.
   Query Match
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NEF_HV1H2
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us-09-509-239-17.rsp

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SEQUENCE FROM N.A.
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.;
                                                                                                                Query Match
Best Local Simil
Matches 120; (
                                                                                                                                                                                                                                                       230 FPD 232
                                                                                                                                                                                                                                                                             121 FPD 123
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Q06282;
                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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-1- MISCELLANEOUS: IN THIS ISOLATE A MUTATION IN POSITION 124 A STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                    170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
                                                                                                                                                                                                                                 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY 120
                                                                                                                                                                        110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                              9
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-85111123; PubMed-2578615;
Statner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumelster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11678;
                                                                                                                           Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of the AIDS virus, HTLV-III.
Nature 313:277-284(1985).
                                                                                                                                                 1; Indels
21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION. MEDLINE-88039140; PubMed-3118220;
                                                                                                                           DB 1;
                                                                                                                         Score 645; DB 1;
Pred. No. 9e-47;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                  123 AA.
                                                                                                                           28.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M15654; AAA44206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 330:266-269(1987).
                                                                                                                                      Best Local Similarity 98.4
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A04005; ASLJH3.
HSSP; Q70627; 2NEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wong-Staal F.;
                                                                                                                                                                                                                                                                  230 FPD 232
                                                                                                                                                                                                                                                                                        FPD 123
                                                                                                                                                                                                                                                                                                                          RESULT 24
NEF_HV1B1
ID NEF_HV1B1
AC P03404;
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                        121
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Glycerophosphoryl diester phosphodiesterase precursor (EC 3.1.4.46)
(Glycerophosphodiester phosphodiesterase) (Surface-exposed lipoprotein
D) (Protein D) (Immunoglobulin D-binding protein) (IGD-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MINNA / SEROTYPE B;
MEDLINE=940113156; PubMed=8104899;
Janson H., Ruan M., Forsgren A.;
"Limited diversity of the protein D gene (hpd) among encapsulated and nonencapsulated Haemophilus influenzae strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QEEEEVGFPVTPQVPLRPMTYKAANDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTGGY 120
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STRAIN=RD, KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Weidman J.E., Shirley R., Liu L.-II., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hannam M.C., Nguyen D.T., Sauddek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DECULNIA 772;
MEDLINE-91099948; pubMed-1987023;
MEDLINE-91099948; pubMed-1987023;
Janson H., Heden L.-O., Grubb A., Ruan M., Forsgren A.;
Janson H., Heden L.-O., Grubb A., Ruan M., Forsgren A.;
"Protein D, an immunoglobulin D-binding protein of Haemophilus influenzae: cloning, nucleotide sequence, and expression in
                                                                                                                                                                                                                                                                                                                                                                           ;
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Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                    2 2 MYRISTATE.
123 AA; 13606 MW; 0811735345F0EB8B CRC64;
                                                                                                                                                                                                                                                                                             11arity 97.6%; Pred. No. 3.4e-46; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 AA
HIV; M15654; NEF$BH102.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS: Myristate; GTP-binding.
LIPID 2 2 MYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae
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                                                                                                                           Conservative
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Nature 313:277-284(1985)
 253
310
327
                                          338
                                                               364
                                                                        364 AA;
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel.
                                                                                                                                                                                                                                                                                                                                                           E---PDKV 262
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 253
310
327
                                          338
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13-AUG-1987 (
16-OCT-2001 (
                                                                                                      Query Match
Best Local Simi
Matches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 TAT_HV1B1
P04606;
                                                                        SEQUENCE
VARIANT
VARIANT
VARIANT
                                          VARIANT
                                                               VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                            DR EMBL; M37487; AAA24998.1; -
DR EMBL; M37487; AAA24998.1; -
DR EMBL; 235656; CAA84716.1; -
DR EMBL; 235659; CAA84716.1; -
DR EMBL; 235659; CAA8477.1; -
DR EMBL; 235659; CAA8477.1; -
DR EMBL; 235660; CAA8477.1; -
DR EMBL; 235660; CAA8477.1; -
DR PRBL; 235661; CAA84719.1; -
DR TIGR; H10689; -
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
R PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
R Qlycerol metabolism; Hydrolase; Signal; Lipoprotein; Outer membrane; W Complete proteome.
T SIGNAL
                                                                                                                                                                                                                                                            PTM: CONTAINS BOTH ESTER- AND AMIDE-LINKED FATTY ACIDS.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS NTHI 772 AND
                                                                                                            PHOSPHODIESTERASE.

N-ACYL DIGLYCERIDE.

L -> V (IN STRAIN NCTC 8468).

L -> V (IN STRAIN NCTC 8468).

N -> S (IN STRAIN NCTC 8468).

N -> S (IN STRAIN NCTC 8468).

D -> H (IN STRAIN NCTC 8468).

H -> O (IN STRAIN 8-7626).

C -> O (IN STRAINS EAGAN; 3639; 3640;

C -> O (IN STRAINS EAGAN; 3639; 3640;

NCTC 8468; 6-7626; HK695; MINNA).

Y -> H (IN STRAINS EAGAN; 3639; 3640;

NCTC 8468; 6-7626; HK695; MINNA).

Y -> H (IN STRAIN NCTC 8468).

K -> O (IN STRAIN 6-7626;

K -> O (IN STRAIN 6-7626;

K -> A (IN STRAIN 6-7626).

T -> A (IN STRAIN 6-7626).

T -> A (IN STRAIN 6-7626).

NCTC 8468; 6-7626; HK695; MINNA).

NCTC 8468; 6-7626; HK695; MINNA).
                                                                                                                                                                                                                   CATALYTIC ACTIVITY: A glycerophosphodiester + H(2)0 - an alcohol
                                                                                                                                                                                                                              sn-glycerol 3-phosphate.
SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                  Song X.-M., Forsgren A., Janson H.;
"The gene encoding protein D (hpd) is highly conserved among
Heamophilus influenzae type b and nontypeable strains.";
Infect. Immun. 63:696-699(1995).
                              8468, 6-7626, AND HK695;
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                                                                                                                                                                                                                                                                                         SIMILARITY: TO E.COLI AND B.SUBTILIS GLPQ
                 SEQUENCE FROM N.A.
STRAIN-EAGAN, 3639, 3640, NCTC 84(
MEDLINE-95122210; PubMed-7822043;
Infect. Immun. 61:4546~4552(1993)
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144
168
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P -> S (IN STRAIN 6-7626).

Q -> K (IN STRAIN 6-7626).

E -> A (IN STRAINS EAGAN; 3639; NCTC

8468; 6-7626; HK695; MINNA).

A -> V (IN STRAINS EAGAN; 3640; HK695;

MINNA).

K -> E (IN STRAIN 6-7626).
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SERIN-ISOLATE HXB3;
MEDLINE-85228248, PubMed-2988795;
Crowl R., Ganquly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;
HTUV-III env gene products synthesized in E. coll are recognized that thooles present in the sera of AIDS patients.";
Cell 41:979-986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRL
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STRAIN-ISOLATE BHIO;
MEDLINE-85111123; PubMed-2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumelster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.
                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                          1; Length 364;
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                                                                                                                                                                                                                                                                                                                   24.9%; Score 562.5; DB 1; Length 46.1%; Pred. No. 2.6e-39; Live 21; Mismatches 72; Indels
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A6079B3ABF70E820 CRC64;
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13-AUG-1987
16-OCT-2001
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P04326;
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Nature 313:450-458(1985)
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
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Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ranscription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                         1- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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                                                                  SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR
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                                                                                                                                                                                                                                                                                                                                                        EMBL; M14100; AAA44676.1; -.
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HIV; M14100; TAT$HXB3.
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es 85; Conserva
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P04607;
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MEDLINE=86177573; PubMed-3008154;

Arya S.K., Gallo R.C.;

Three novel genes of human T-lymphotropic virus type III: immune reactivity of thair products with sera from acquired immune deficiency syndrome patients.";

Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986);

Proc. Natl. RANSCRIPTIONAL REGULANOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMBYT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                 Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                       Length 86;
                                                                                                                                                                                                                                                                                                                                                                       Score 481; DB 1; Length 86 Pred. No. 2.3e-33; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (clone 12) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                    86 AA; 9794 MW; 4DD5C6415FAF9015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                            EMBL; X01762; ·; NOT_ANNOTATED_CDS HIV; K02083; TAT$PV22.
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(Rel. 40, Last anno
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HIV; M11840; TATSPCY12.
InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                     HIVTATDOMAIN
                                                                                           InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                                                       21.3%;
98.8%;
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EMBL; K02083; AAB59870.1;
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DB 1; Length 86;

Score 478;

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                                                                                                                                                                                                                                                                                                                                                                BUCKLET C.E., BUCKLET-White A.J., Willey R.L., MCCOY J.;
Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY EINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) THA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                          EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 377
                      Gaps
                                                      2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRAPGG 61
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T -> M (IN CLONE PNL4-3).
PPOG -> AHON (IN CLONE PNL4-3).
V -> A (IN CLONE PNL4-3).
P -> S (IN CLONE PNL4-3).
9B1B4A915FAF8A14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 470; DB 1; Length 86; Pred. No. 1.9e-32; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                numan immunodeficiency virus type 1 (BRU isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
(1)
                                                                                                                                                                                                                                                                                                  MEDLINE-85099333; PubMed-2981635; Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.; Wain-Hotide sequence of the AIDS virus, LAV."; Cell 40:9-17(1985).
                      Indels
. 4.1e-33;
                                                                                                                                                                                                                      TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                Last sequence update)
Last annotation update)
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         Pred. No. 4.1e
0; Mismatches
                                                                                     378 SQTHQVSLSKQPTSQSRGDPTGPKE 402
                                                                                                                                                                                                                                                                                                                                                         (CLONE PNL4-3).
                                                                                                SQTHQVSLSKQPTSQSRGDPTGPKE
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96.5%;
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                      Conservative
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Best Local Similarity
Matches 82; Conserv
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         | Similarity
84; Conser
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16-OCT-2001
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P04610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDS.";
Cell 45:637-648(1986).
1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F., "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 461; DB 1; Length 102;
Pred. No. 1.3e-31;
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                                                                                                                                                                                                                                                                                                                                               (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                    102 AA
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                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-86218077; PubMed-2423250;
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                                62 SQTHQVSLSKQPTSQPRGDPTGPKE
SQTHQVSLSKQPTSQSRGDPTGPKE
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(Rel. 09, Last sequ
(Rel. 40, Last anno
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Best Local Similarity 91.9%;
Matches 79; Conservative
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01-NOV-1988
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                               TAT protein
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P05908;
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378
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EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 377

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170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A., Johansson B., Vahine A., Sonnerborg A.;
"HIV-1 nef mutations and clinical long-term non progression: a molecular epidemiology study.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP: P03406: LEFN.
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Pfam, PR00469; F-protein; 1.
AlDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23328 MW; FCC69458158F1A03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE PACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retrold viruses; Retroviridae; Lentivirus
NCBL_TaxID=11676;
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Pred. No. 2.7e-83;
1; Mismatches 0;
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090597
09W7X2
090594
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Q9DQT9
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  Best Local Similarity
Matches 205; Conser
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                                                                                                                                                                                                                                                                                                         molecular epidemiology study.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF047087; AAD02461.1; -- HSSP; P03406; 1EFN.
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Pred. No. 6.9e-83;
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Last sequence update)
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(27 KDA PROTEIN)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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AIDS; GTP-binding; Myristate.
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Matches 204; Conservative
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MEDLINE=96036482: PubMed=7483282;
Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
Recovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
Virology 213:80-86(1995).
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                                                                                                                                                                                                                                                                                                       "Constructing full-length chimeric HIV-1 molecular clones by PCR-
"Constructing full-length chimeric HIV-1 molecular clones by PCR-
mediated recombination.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; 1EFN.
InterPro; IPR001558; F-protein.
InterPro; IPR001558; F-protein.
AIDS; GTP-Dinding; Myristate.
SEQUENCE 206 AA; 23428 MW; 9F94AEB9CAFDC6F6 CRC64;
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J. Virol. 59:284-291(1986).
EMBL: UZ6942; AAB66579.1; .
SEQUENCE 206 AA; 23367 MW; 65AF3B6184DC2FE7 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.7e-82;
!; Mismatches 2;
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ilarity 98.5%;
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Last sequence update) Last annotation update)

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12,

206 AA

PRT;

(27 KDA PROTEIN).

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molecular epidemiology study.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: NEF HAS GTPASE, GPP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF011494; AAD01472.1; -.
                                                                                                                                                              Visco Comandini U., Yun 2., Paganelli R., Orlandi P., Salotti ,
Johansson B., Vahlne A., Sonnerborg A.;
"HIV-1 nef mutations and clinical long-term non progression: a
                                                                                                  Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11676;
                                                                                        Human immunodeficiency virus
                                                               NEGATIVE FACTOR (F-PROTEIN)
     PRELIMINARY;
                                         (TrEMBLrel.
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                            01-NOV-1999
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                                                                                               230 FPDWONYTPGFGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
121 FPDWONYTPGFGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                 110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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   Length 206;
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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 Score 1115; DB 15;
Pred. No. 3.7e-82;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                         206 AA.
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23454 MW;
49.4%;
llarity 98.1%;
Conservative
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AIDS 6:1427-1436(1992).
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Best Local Similarity
Matches 200; Conserv
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202; Conser
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(27 KDA PROTEIN)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                  Score 1105; DB 15;
Pred. No. 2.3e-81;
2; Mismatches 4;
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23333 MW;
                                                                                                                  Query Match
Best Local Similarity 97.1%;
Matches 200; Conservative
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SEQUENCE FROM N.A.
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Aids-associated retrovirus
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Kohleisen B., Neumann M., Herrmann R., Brack-Werner R., Krohn K.J.,
Ovod V., Ranki A., Erfle V.;
"Cellular localization of Nef expressed in persistently HIV-1-infected
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AIDS 6:1427-1436(1992).
--- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
--- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
--- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
HSSP; P03406; 1EFN.
                                                                                                                                                              110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                 170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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Pfam; PF00469; F-protein; 1.
AIDS: GTP-binding; Myristate.
SEQUENCE 206 AA; 23439 MW; 8478CF194D39D5B9 CRC64;
                                                             0ED69927C2E03BB6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE PACTOR (F-PROTEIN) (27 KDA PROTEIN)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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ilarity 96.1%; Pred. No. 4.9e-81;
Conservative 4; Mismatches 4;
                                                                                               Query Match 49.0%; Score 1104; DB 15; Best Local Similarity 97.1%; Pred. No. 2.8e-81; Matches 200; Conservative 1; Mismatches 5;
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EMBL; AF011469; AAD01447.1; -. HSSP; P03406; IEFN.
INTERPRO; IPRO1558; F-protein.
Pfam; PF00469; F-protein; I.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23345 MW;
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Best Local Simi
Matches 198;
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                                                                                                                                                                                                                                                                                                                                                                                     Fang H., Pincus S.H.;
Fang H., Pincus S.H.;
Spontaneous activation of human immunodeficiency virus type 1 in an immunotoxin-resistant variant T cell line.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SERMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.
EMBL; AFO70521: AAC28453.1; --
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Fang H., Pincus S.H.;
Unique insertion sequence and pa
selected with immunotoxins from h
infected T cells.";
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Pfam; PF00469; F-protein; J.
AIDS; GTP-binding; Myristae.
SEQUENCE 206 AA; 23334 MW;
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                                                             01-NOV-1998 (TremBLrel. 08, 01-DEC-2001 (TremBLrel. 19, NEGATIVE FACTOR (F-PROTEIN)
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      PRELIMINARY;
                                          01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Best Local Simi
Matches 197;
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01-DEC-2001
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FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecular epidemiology study.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1988) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL. ARG47084; AAD02458.1;
-- HSSP: P03406; LEPA
                                                                           frt. J. Immunopharmacol. 3:17-23(1990).
-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(F4) ANTIGEN.
EMBL; 211530; CAA77629 1; -
HSSP; P03406; 1EFN.
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                                                                                                                                                                                   Interpro; IPR001558; F-protein.
Pfam, PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23398 MW; A31CC7244BBB2B43 CRC64;
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NCBL_TaxID=11676;
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Last annotation update)
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Pred. No. 2.6e-80;
7; Mismatches 2;
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Pred. No. 1.2e-80;
3; Mismatches 4;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence upd
01-DEC-2001 (TrEMBLrel. 19, Last annotation u)
06ARIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
             Borsetti A., Saggio I., Verani P., Rossi G.;
"Variability of HIV-1 virus: characteristics
productive clone.";
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23512 MW;
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Best Local Similarity 96.6%;
Matches 199; Conservative
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Best Local Similarity 95.6
Matches 197; Conservative
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                                                                                        MEDLINE-86667228; PubMed-2999715;
Ratner L., Starcich B., Josephs S.F., Hahn B.H., Reddy E.P.,
Livak K.J., Petteway S.R.Jr., Pearson M.L., Haseltine W.A., Arya S.K.,
Wong-staal F.;
"Polymorphism of the 3' open reading frame of the virus associated
with the acquired immune deficiency syndrome, human T-lymphotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 MGCKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus type III.";
Nucleic Acids Res. 13:8219-8229(1985).
--- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
--- SIMILARITY: DEFMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; X01188; CAAA26947.1; ---
HSSP; P03406; 1EFN.
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MEDLINE-89352106; PubMed-2765297;
Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B. Macchi B., Manglano N., Verani P., Rossi G.;
Macchi B., Manglano N., Verani P., Rossi G.;
"Biological and molecular characterization of producer and non producer clones from HUT-78 infected with a patient HIV isolate.";
AIDS Res. Hum. Retroviruses 5:385-396(1989).
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Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo
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Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Verahi P., Rossi G.B.;

"Sequence analysis of HIV-1 proviral DNA from a non producer chronically infected HUT-78 cellular clone.";
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Pfam: PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEOUENCE 206 AA; 23419 MW; 3B25EB332A479A46 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae.
NCBI_TaxID=11966;
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                                                                        SEQUENCE FROM N.A.
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Length 206;

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Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
(27 KDA PROTEIN).
                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                 48.3%; Score 1090; DB 15;
95.1%; Pred. No. 3.8e-80;
Live 6; Mismatches 4;
                                                                                                                          206 AA.
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                                                                           191 LEWRFDSRLAFHHVARELHPEYYKNC 206
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                                                                    LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                   interPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                          Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23617 MW;
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Q89561;
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N [1] N [1] N A. Arens N.A. A Arens M.O., Ratner L., Joseph T., Bandres J.; Arens M.O., Ratner L., Joseph T., Bandres J.; Arens M.O., Ratner L., Joseph T., Bandres J.; Submitteed (JAN-1996) to the EMBL/GenBank/DDBJ databases.

1. Submitteed (JAN-1996) to the EMBL/GenBank/DDBJ databases.

2. -i. SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR REBL: U44448; AAB38109.1; -.

DR REBL: U44447; AAB38199.1; -.

DR RICHARD: IPRO01558; F-protein.

DR RICHARD: Prodein; 1.

KW AIDS, GTP-binding; My1state.

**CATIFICE** 206 AA; 23629 MW; BF467FB1B7147CDE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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Pred. No. 6.6e-80; 7; Mismatches 4; Indels 0
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Last sequence update)
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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95.6%; Pred. No. 9.6e-80;
iive 5; Mismatches 4
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InterPro; IPR001558; F-protein.
Pfam: PF00469; F-protein: 1.
AIDS; GTP-binding; Myristate.
SEOUENCE 206 AA; 23649 MW;
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94.78;
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Matches 195; Conservative
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Best Local Similarity
Matches 196; Conserv
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WEDLINE-96400183; PubMed-8806559;
A Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A.,
A Hahn B., Powderly W., Arens M.;
T "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects
T "Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects
T tdifferent stages of disease.";
Virology 223:245-250(1996).
T SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
T SIMILARITY: IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

BASP: P03406; IEFN.
THEOPRO; IPRO01558; F-protein.

A HSSP: P04465; F-protein.

BR Ffam: PF004669; F-protein.

A AIDS; GTP-binding; Myristate.
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InterPro; IPR001558; F-protein.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 2.9e-79;
5; Mismatches 5;
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Matches 195; Conservative
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                                                                                                NCBI_TaxID=11676;
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Q74915;
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               170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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Pred. No. 2.4e-79;
5; Mismatches 6; Indels 0;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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94.78;
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Best Local Similarity 94.7
Matches 195; Conservative
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Length 206; Indels

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                                                                                                                                            170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
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                                                                10 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
                                                                                                        170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
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                                               Gaps
                                                                            -!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTYTIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN. EMBL; U44449; AAB38201.1; -- HSSP; Q70627; ZNEF.
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Pfam. PF00469; F-protein. 1.
AlDS: GTP-binding; Myristate.
SEQUENCE 206 AA; 23488 MW; F0S96D6FAAA81A05 CRC64;
ESBD6FA0B70FC175 CRC64;
                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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                         Score 1079; DB 15;
Pred. No. 2.9e-79;
5; Mismatches 4;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
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                         47.8%;
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01-DEC-2001 (TrEMBLrel. 19, 1
NEGATIVE FACTOR (F-PROTEIN)
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Matches 194; Conservative
                           Ouery Match
Best Local Similarity 95.6
Matches 195; Conservative
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206 AA;
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Piedade J., Esc. 1.

A Canas-Ferreira W.F.;

A Canas-Ferreira W.F.;

RT "Cloning and expression of HIV-1 nef gene in the carrier-adjuvant

RT pVUB3 expression system based on the major lipoprotein (OprI) from the

RT outer membrane of Pseudomonas aeruginosa.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR RSSP; P03406; 1EFN.

DR HSSP; P03406; 1EFN.

InterPro; 1PR001558; F-protein.

DR HSSP; P04469; F-protein.

RW AIDS; GTP-binding; Myristate.

FT NON_TER 202 202
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Wang B., Saksena N.K.;
"HIV-1 Strains from a cohort of American subjects reveal the presence
of a V2 region extension unique to slow progressors and non-
progressors.";
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                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN) (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 5e-79;
0; Mismatches 5;
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SEQUENCE FROM N.A.
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ACTIVITIES, IT SEEMS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN. HSSP, PO34065, 1EFN.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 1.1e-78;
5; Mismatches 8;
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Pred. No. 1.1e-78;
2; Mismatches 9;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23420 MW;
                                                                                                                              InterPro: IPR001558; F-protein. Pfam: PF00469; F-protein; 1. AIDS; GTP-binding; Myristate. SEQUENCE 206 AA; 23510 MW;
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93.7%;
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Best Local Similarity 94.7%;
Matches 195; Conservative 2
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Matches 193; Conservative
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                      110 MGGKWSKSSVVGWPTVRERMRRAEPA--ADGVGAASRDLEKHGAITSSNTAAINAACAWL 167
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Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,
Johansson B., Vahline A., Sonnerborg A.;
HIV-1 nef mutations and clinical long-term non progression: a
molecular epidemiology study.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN.
HSSP; P03406; LEFN.
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230 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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AIDS; GTP-binding; Myristate.
SEQUENCE 208 AA; 23681 MW; 1C891C3AD230C6A8 CRC64;
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Last annotation update)
(27 KDA PROTEIN).
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.3e-78;
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Similarity 94.28;
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
01-DEC-2001 (TrEMBLrel, 19,
NEGATIVE FACTOR (F-PROTEIN)
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                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            pediatric long-term survivors.;
AIDS Res. Hum. Retroviruses 16:1855-1868(2000).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; 1EFN
                                                                          J. Neurovirol. 4:0-0(1998).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; 1EFN.
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MEDLINE-21002575; PubMed-11118071;
MEDLINE-21002575; PubMed-11118071;
MEDLINE-21002575; PubMed-11118071;
Saspide C., Wolf D., Muller R., Hill M.D., Stellwag E., Freitag M., Sass G., Scott G.B., Baur A.S.;
"Functional and structural defects in HIV-1 nef genes derived from
SEQUENCE FROM N.A.
STRAIN-PATIENT 27;
STRAIN-PATIENT 27;
Perbee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of Propositive individuals/AIDS patients with or without AIDS dementia
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U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA.
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NCE 206 AA; 23464 MW;
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23499 MW;
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AIDS, GTP-binding, Myristate.
SEQUENCE 206 AA.
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090QU1;
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Q9DQU1
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110 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 169
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-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL: AF064675; AAC1876.1; -
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STRAIN-PATIENT 27;
STRAIN-PATIENT 27;
PERPRED D.A., Greenway A.L., Holloway G., Smith K., Deacon N., Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of H positive individuals/AIDS patients with or without AIDS dementia
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Pred. No. 4.7e-78;
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; I.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23514 MW; C
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91.78;
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HSSP; P03406; 1EFN.
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Length 206;

Query Match 47.2%; Score 1065; DB 15; Best Local Similarity 93.2%; Pred. No. 3.9e-78; Matches 192; Conservative 9; Mismatches 5;

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ACTIVITIES, IT SEEMS TO EMBL; AF064673; AAC18374.1; HSSP; P03406; LEFN.
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SEQUENCE FROM N.A.
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01-MAY-2000 (
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STRAIN-PATIENT 27;
McPhee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemborton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of HIV-
I positive individuals/AIDS patients with or without AIDS dementia
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J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 17:58-68(1998).
I- SIMILARITY: NF FANS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITES, T SERMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
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Last sequence update)
Last annotation update)
(27 KDA PROTEIN)
                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                         Viruses, Retroid viruses, Retroviridae, NCBI_TaxID=11676;
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MEDLINE-98097260; Pubmed-9436760;
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SEQUENCE 206 AA; 23348 MW;
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                                             (TrEMBLrel. 08, (TrEMBLrel. 08,
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    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         progressors.";
AIDS 0:0-0(2000).
-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-XIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
--- SAMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHORYLATING
--- SAMILARITY: NEF HAS GTP-BINDING AND AUTOPHORYLATING
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DOWN-REGULATE THE CD4 (T4) ANTIGEN
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                                                                                                                                                                                                                                             2255A447ECE85456 CRC64;
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                          47.1%; Score 1061; DB 15;
91.7%; Pred. No. 8.2e-78;
tive 12; Mismatches 5;
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Pred. No. 9.9e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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"HIV-1 Strains from a cohort of
of a V2 region extension unique
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myxistate.
SEQUENCE 206 AA, 23599 MW;
                                                                                                                InterPro: IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 As: 23472 MW;
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92.7%;
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STRAILPATIENT 27;
MCPhes D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of HIV-
I positive individuals/AIDS patients with or without AIDS dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     J. Neurovirol. 4:0-0(1998).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; AF064677; AAC18378.1; --
HSSP; P03406; 1EFN.
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Query Match

46.9%; Score 1057; DB 15; Length 206;
Best Local Similarity 91.3%; Pred. No. 1.7e-77;

Matches 188; Conservative 13; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DC6A96AF05891D6B CRC64;
                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID-11676;
                                                                                                                                         206 AA
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Job time: 384 sec
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                             290 LEWRFDSRLAFHHVARELHPEYFKNC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00469; F-protein: 1.
AIDS; GTP-binding; Myristate: SEOUENCE 206 AA; 23442 MW;
                                                                                                                                       PRELIMINARY;
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01-NOV-1999 (
01-NOV-1999 (
01-DEC-2001 (
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AAY02355 standard; Protein; 413 AA.
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/ SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:*
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2264
1 MDPSSHSSNMANTQMKSDKI......QSRGDPTGPKETSGHHHHHH 413
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAY02352
AAG63234
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AAG63233
AAY02357
                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Amino acid sequenc A representative H Amino acid sequenc Human NEF protein/ Nef protein of HIV HIV-1 nef protein. HIV-1 nef protein Sequence of E' pro Sequence of E' pro	rfl Nef potral oct CRL rfl Nef potral ATCC CRL rfl Nef (train OYI PA leader PA leader	1 non-subtyp 1 subtype C 1 non-subtyp ance encoded 1 non-subtyp lence deduced 1 non-subtyp	HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype HIV-1 strain YBF30
AAG63239 AAY02349 AAG6231 AAY50795 AAR38893 AAB10054 AAB155 AAP61515	AAW90P79 AAE04860 AAW51113 AAY77299 AAE04962 AAE04962 AAE04961	AAB6933 AAB69361 AAB69361 AAB69359 AAR08407 AAB69364	AAB69362 AAB69365 AAB69366 AAB69357 AAB69358 AAB69360 AAW72998 AAP81866 AAW68481
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## ALIGNMENTS

HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein; vaccine; HIV infection; protein D. HIV Tat or Nef protein linked to a fusion partner A representative LipoD-Tat fusion protein. (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. Human immunodeficiency virus type 1. Marchand M; 98WO-EP06040. 97GB-0020585 (first entry) Bruck C, Godart SAG, WPI; 1999-302282/25. N-PSDB; AAX35691.

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    The present sequence represents a fusion protein comprising LipoD-HIV-1 Tat. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.
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                                                                               Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                          tat gene; vaccine; gpl20 gene; HIV viral load
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; Pred. No. 3.1e-205;
0; Mismatches 0;
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/note= "ProtD fusion
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2000GB-0013806.
2000WO-EP05998.
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                                                                                       Local Similarity 100.
nes 413; Conservative
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06-JUN-2000;
28-JUN-2000;
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Best Local Si
Matches 413;
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The present sequence represents a His-tagged ProtD-Nef-Tat fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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le and an HIV gp120
a vaccine -
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100.0%; Pred. No. 3.1e-205;
ive 0; Mismatches 0;
                                                                                                                                                                              New use of a human immunodeficiency virus (HIV) Ta
linked to Tat (Nef-Tat) protein or polynucleotide
protein or polynucleotide for the manufacture of a
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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N-PSDB; AAH42881.
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Matches 413;
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64 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG 123
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Matches 409; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a His-tagged Nef-Tat linked protein of HIV, with a lipidation signal sequence (LipoD) which is removed after processing and a ProtD fusion partner. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat
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                                                                                                                                                                                                                                                                                                                                                      New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
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100.0%; Pred. No. 1.5e-203;
1ve 0; Mismatches 0;
                          Location/Qualifiers
1..109
/note= "ProtD fusion partner"
                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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immunodeficiency virus
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14-APR-2000; 2000GB-0009336.
06-JUN-2000; 2000GB-0013806.
28-JUN-2000; 2000WO-EP05998.
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Best Local Similarity 100.
Matches 410; Conservative
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Gaps 63

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Length 411; Indels

Score 2233; DB 20; Pred. No. 2.6e-202; ); Mismatches 1;

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The present sequence represents a fusion protein comprising Lipob-HIV-1 Tat-His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                      gene; Nef protein; Tat protein;
HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                               A representative LipoD-Tat-His fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                   nef gene; fusion protein; HIV
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us-09-509-239-21.rag

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GPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRL
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Best Local Similarity
                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFP 180
        HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI 363
                                                                                                                                                         gene; Nef protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 326;
                                Indels
                                                                                                                                                                                                                                                                                                                                 HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1715,5; DB 2
Pred. No. 1.5e-153;
0; Mismatches 0;
                                                                                                                                        A representative LipoD-Nef fusion protein.
                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                        HIV nef gene; fusion protein; HIV nef vaccine; HIV infection; protein D.
                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                        AAY02354 standard; Protein; 326 AA
                                                                                                                                                                                                                                                                                         Marchand M;
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.8%;
Best Local Similarity 78.9%;
Matches 326; Conservative
                                                                                                                                                                                                                                         98WO-EP06040
                                                                                                                                                                                                                                                        97GB-0020585
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                         Godart SAG,
                                                                                                                                                                                                                                                                                                       WPI; 1999-302282/25.
N-PSDB; AAX35690.
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                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                                                                                         17-SEP-1998;
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                                                                                                                                                                                                        WO9916884-A1
                                                                                                                         09-JUL-1999
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                                                                                                        AAY02354;
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304
                                                                                 AAY02354
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The present sequence represents a His-tagged ProtD-Nef fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
241 gpgvrypltfgwcyklvpvepdkveeankgentsllhpvslhgm&dperevlewrfdsrl 300
                                                                                                                                                         317
                                                                                              AFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or Nef
gp120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tagged ProtD-Nef fusion protein
                                                                                                                                                                                                                       361 LGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG63236 standard; Protein; 326
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2000GB-0009336.
2000GB-0013806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                  WPI; 2001-476172/51.
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06-JUN-2000;
28-JUN-2000;
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Length 326;

Score 1715.5; DB 22; Pred. No. 1.5e-153;

75.8%; 78.9%;

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Length 324;

DB 20;

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N-PSDB; AAH42878
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28-JUN-2000;
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                                                                  Best Local Sim
Matches 323;
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                                               Query Match
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; Nef protein; Tat protein;
      Gaps
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                                        MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAOOADYLEODLAMTKDG
                                                                VTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTP
                                                                                                                                                                                                                                                                                                            GPGVRYPLIFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRL
      87;
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-----tsghhhhhh 326
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  Mismatches
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  Conservative
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N-PSDB; AAX35688.
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Matches 326;
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                                    63
                                                     61
                    Gaps
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                                                                      VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG
                                                                                                           4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                              VRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFH
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                   87;
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                                                                                                                                                                                                                                                                                324
                   Indels
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                                                                                                                                                                                                                                                              364 SYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New use of a human immunodeficiency virus (HIV) Tat,
                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a His tagged LipD-Nef of HIV.
                   ö
          .5e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..109
/note= "ProtD fusion partner"
Score 1697.5;
Pred. No. 7.5e
                  Mismatches
          Pred. No.
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                                                                                                                                                                                                                                                                                                                              AAG63234 standard; Protein; 324
75.0%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000GB-0002200.
2000GB-0009336.
2000GB-0013806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-EP05998
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
        Similarity 78.83
23; Conservative
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                                                                     The present sequence represents a His-tagged Nef protein of HIV, with a lipidation signal sequence (LipO) which is removed after processing. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat. HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophlactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV-gpl20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGI 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                  VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSSVVG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                   61
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSHSSNMANTOMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                                                                                                                                                                                                                                                                                                                                                        QVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPG
                                                                                                                                                                                                                                                                                                DB 22; Length 324;
                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 413
                                                                                                                                                                                                                                                                                             Score 1697.5; DB 22; Lengthered, No. 7.5e-152;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; Nef
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV nef gene; fusion protein; HIV nef vaccine; HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Human immunodeficiency virus type
                                           Disclosure, Fig 1, 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02351 standard; Protein; 302
                                                                                                                                                                                                                                                                                             tch 75.0%;
al Similarity 78.8%;
323; Conservative
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Best Local Similarity
Matches 323; Conserv
                                                                                                                                                                                                                                                      324 AA;
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The present sequence represents a representative HIV-1 Nef-Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                             112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                             172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                  FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                              LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSOPKTACTNCYCKKCCFH
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                                                                                                                                                                                                                                                 Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a His-tagged Nef-Tat linked
                                                                                                                                                                                                                                                 74.6%; Score 1688; DB 20;
ilarity 100.0%; Pred. No. 5.4e-151;
Conservative 0; Mismatches 0;
                                                                                                                    HIV Tat or Nef protein linked to a fusion partner
                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                        Disclosure; Fig 2; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus
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                     97GB-0020585
                                                                                    WPI; 1999-302282/25
N-PSDB; AAX35687.
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Best Local Similarity
Matches 302; Conserv
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                     26-SEP-1997;
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17-SEP-1998;
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                                                              Bruck C,
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                                                                                                                                                                                 The present sequence represents a His-tagged Nef-Tat linked protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat. HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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                                                                                                                                                                                                                                                                                                                                                                                                               231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                      New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
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                                                                                                                                                                                                                                                                                                                               Length 302;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                              74.6%; Score 1688; DB 22;
100.0%; Pred. No. 5.4e-151;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; Nef
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                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                Disclosure; Fig 1; 90pp; English
         2000GB-0009336.
2000GB-0013806.
                            28-JUN-2000; 2000WO-EP05998
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                                                                                                                                                                                                                                                                                                                              Query Match 74.6
Best Local Similarity 100.
Matches 302; Conservative
                                                                                        WPI; 2001-476172/51.
N-PSDB; AAH42877.
                                                                                                                                                                                                                                                                                                 302 AA
         14-APR-2000;
06-JUN-2000;
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The present sequence represents a representative HIV-1 mutant Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV
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                                                                                                                                                                                                                                                                                                   HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1675; DB 20;
Pred. No. 9.1e-150;
2; Mismatches 1;
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Synthetic.
Human immunodeficiency virus
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                                                                                                                                                   26-SEP-1997;
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                                                WO9916884-A1
                                                                                 08-APR-1999,
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hh 302
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AAY02349 standard; Protein; 215
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                                                                                                                                                                                                                                                                                                                                                                                     The protein is expressed in the yeast Pichla pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV 9p120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                           New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a His-tagged mutant His protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COVCFITKALGISYGRKKRRORRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 1675; DB 22; Length 302; 99.0%; Pred. No. 9.1e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 90pp; English.
                                                                                                                                             2000GB-0009336.
2000GB-0013806.
2000WO-EP05998.
                           Human immunodeficiency virus
                                                                                                        29-JAN-2001; 2001WO-EP00944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                     WPI; 2001-476172/51.
N-PSDB; AAH42883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 299; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 AA;
                                                     WO200154719-A2
                                                                                                                                              14-APR-2000; 2
06-JUN-2000; 2
28-JUN-2000; 2
                                                                                                                                   31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
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                                                                              02-AUG-2001
                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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The present sequence represents a representative HIV-1 Nef-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-1 Tat protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSOPKTACTNCYCKKCCFH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                            nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein; cine; HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1139.5; DB 20; Length
Pred. No. 2.3e-99;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                       representative HIV-1 Nef-His protein.
                                                                                                                                                                                                                                                                                                                                                                                                                      Marchand M;
                                                                                                                                                                  Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 2; 66pp; English.
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71.2%;
                                                                                                                                                                                                                                                                                             98WO-EP06040
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Godart SAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-302282/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX35685
                                                                                                                                                                                                                                                                                                                                     26-SEP-1997;
                                                                                                                                                                                                                                                                                               17-SEP-1998;
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09-JUL-1999
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                                                                                                                                                Synthetic.
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Best Local S
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This invention describes novel binding partners (A).(1) for negative factor protein (Nef) that competitively inhibit binding of calmodulin (I) to Nef, or (11) for (I) that competitively inhibit binding of Nef to (I). (A) are used for prevention, diagnosis (by specific detection of intraand/or extra-callular Nef, including staging of infection), and/or treatment of infections with human immune deficiency virus (HIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention and diagnosis of human
                                                                                                                                                                                                                                                                                                        binding inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                        NEF protein; calmodulin; negative factor protein; diagnosis; detection; infection; treatment; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1120; DB 21;
Pred. No. 1.5e-97;
0; Mismatches 2;
                                                                                                                                                                                                                                                                        Human NEF protein/calmodulin binding inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding agents used for treatment, immune deficiency virus infection
                                                                                                                                                                     AAY50795 standard; protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antz C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 1; 29pp; German.
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                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038789/03
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Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCHO/) SCHOTT M
(SCHO/) SCHORR J
(ANTZ/) ANTZ C.
                                                                                                                                                                                                                                         17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                         WO9957136-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1999
                                                                                     215
                                                     HH 413
                                                                                                                                                                                                        AAY50795;
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                                                                          11
214 hh
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                      207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a His-tagged Nef protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat. HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 215;
                                                                                                                                                    HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
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Pred. No. 2.3e-99;
0; Mismatches 0; Indels
                                                                                                                 Amino acid sequence of a His-tagged Nef protein of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                 AAG63231 standard; Protein; 215 AA
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71.2%;
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2000GB-0009336.
2000GB-0013806.
2000WO-EP05998.
                                                                                                                                                                                                   Human 1mmunodeficiency virus
                                                                                                                                                                                                                                                                                                  29-JAN-2001; 2001WO-EP00944
                                                                                     (first entry)
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Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-476172/51.
N-PSDB; AAH42875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 AA;
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06-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                     31-JAN-2000;
                                                                                 01-OCT-2001
                                                                                                                                                                                                                                                                   02-AUG-2001
                                                                                                                                                                                   Synthetic.
                                                AAG63231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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AAG63231
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(first entry)

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standard; Protein; 206
                                                                HIV-1 nef protein.
                                             02-NOV-2000
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                           AAB10054;
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         AAB10054
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AAB10054
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                                                                                                                                                                                                                                                                                                                                                                         The nef protein comprises peptides which are expressed in vivo in HIV infected patients before detectable amts. of p25, gpl10 and gp41 are expressed. Thus, they can be used in assays for early detection of HI They can also be used to raise antibodies for use in detection, to induce cellular immunity or to raise neutralising antibodies that either inactivate the AIDS virus or reduce the viability of the virus in vivo or destroy infected cells. The peptides may be used in viral vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                            Diagnosis of HIV infection – by detecting HIV antibodies using antigenic polypeptide derived from nef protein of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
                                                                                                                                                                                                                                                                                Montagnier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                AIDS; antibody; p25; gp110; gp41; assay; detection;
immunity; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 49.3%; Score 1116; DB 14; al Similarity 99.0%; Pred. No. 3.5e-97; 204; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                               Ferris S, Granier C,
Sabatier JM;
                                                                                                                                                                                                                                                  (INRM ) INST NAT SANTE & RECH MEDICALE. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 LEWRFDSRLAFHHVARELHPEYFKNC 317
                                      AAR38893 standard; Protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 15pp; English.
                                                                                                                                            Human immunodeficiency virus-1.
                                                                                                                                                                                                     88US-0199143.
                                                                                                                                                                                                                      88US-0199143.
91US-0754300.
                                                                                                                                                                                                                                                                                Bahraoui EM, Chamaret S,
Rietschoten JV, Rochat H,
                                                                           (first entry)
                                                                                             Nef protein of HIV-1.
                                                                                                                                                                                                                                                                                                          WPI; 1993-213434/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 AA;
                                                                                                                                                                                                                      26-MAY-1988;
04-SEP-1991;
                                                                                                                                                                                                     26-MAY-1988;
                                                                           10-NOV-1993
                                                                                                                                                               US5221610-A
                                                                                                                                                                                  22-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                        AAR38893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                   16
                            AAR38893
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This invention describes a novel retroviral packing cell (I), comprising the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV coding gene gp, or a part of these. The products of the invention have anti-HIV and cytostatic activity and can be used for gene therapy. (I) is useful for in vitro infection of cells, especially hematopoletic stem cells, for expression of transgenes in cells and as a pharmaceutical carrier for gene therapy. (I) is therefore useful in the treatment of infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and other diseases. This sequence represents the Human immunodeficiency virus (HIV-1) nef protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New retroviral packing cell useful as pharmaceutical carrier in gene therapy for treatment of HIV and neoplasms, comprises retroviral genes and glycoproteins –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma; nef protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1115; DB 21; Length 206; Pred. No. 4.4e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA40298, AAB10053, AAB10054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 lewrfdsrlafhhvarelhpeyfknc 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                               Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 48; 69pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.2%;
98.1%;
                                                                                                                                                                                                                                                                                                                                   98DE-1056463.
                                                                                                                                                                                                                                                                                                                                                                                       (PETT-) PETTE INST HEINRICH.
                                                                                                                                                                                                                                                                          99EP-0250415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AA;
                                                                                                                                                                                                                                                                             35-NOV-1999;
                                                                                                                                                                                                                                                                                                                                26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   7on Laer MD;
                                                                                                                                                                                                                         07-JUN-2000
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A comparison of AAN60287 with the cDNA of the HTLV-III genome revealed one particular clone, designated p7.11 which contained a DNA sequence encoding this peptide (AAP60308) sequence. This approx. 2.2 kilobase covers the precursor gay region and encodes, 5' to 3', p-12, p-15, p-24 a second p-15 protein, and approx. 300 extra base pairs 3' to the gag region (see AAN60288).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                syndrome polypeptide(s) \frac{1}{1} obtd. by used for diagnosis and in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; immunoassay; HIV; HTLV-IIİ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1111; DB 7;
Pred. No. 1e-96;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of LAV virus ORF F protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.
                             HIV; LAV; AIDS; diagnosis; vaccine.
                                                         HTLV-IIIB/H9 cells (ATCC CRL 8543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 216
                                                                                                                                                                                                                                                                                                                                                                       Example; fig 2; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.1%;
Matches 200; Conservative
                                                                                                                                                                     84US-0685272
85US-0805069
                                                                                                                                            85EP-0309454
                                                                                                                                                                                                                                                                                                             Acquired immune deficiency molecular cloning etc. and against virus disease
 Sequence of E' protein
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                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                           Capon DJ, Lasky LA;
                                                                                                                                                                                                                                                                       WPI; 1986-177602/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA;
                                                                                                                                                                                                                                                                                      N-PSDB; AAN60288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS vaccine;
                                                                                                                                                                     24-DEC-1984;
04-DEC-1985;
                                                                                                                                            23-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1991
                                                                                                                09-JUL-1986
                                                                                     EP187041-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP60423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an antigenic composition comprising an isolated primate lentivitus whose genome contains an engineered non-revertible null mutation in the nef gene, or an infectious DNA clone in a carrier. The antigenic composition is used in vaccines against infection by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231
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                                                                                                                                                                                                                                                                                                                                                                                                                            Lentivirus antigenic compositions - containing lentivirus with nef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                gene; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.2%; Score 1114; DB 20;
llarity 97.6%; Pred. No. 5.4e-97;
Conservative 3; Mismatches 2;
                                                                                                              Antigenic composition; primate; lentivirus; nef infection; AIDS; HIV-1; nef protein.
                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2A-R; 93pp; English
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AAW89326 standard; Protein; 206 AA
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90US-0551945.
91US-0727494.
                                                                                                                                                                                                                                           94US-0188583
                                                                                    HIV-1 nef protein sequence
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                                                        (first entry)
                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE.
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N-PSDB; AAV81866.
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hes 201; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          gene deletion
                                                                                                                                                                                                                                           27-JAN-1994;
                                                                                                                                                                                                                                                                                                 09-JUL-1991;
                                                                                                                                                                                   US5851813-A.
                                                                                                                                                                                                                                                                     27-JAN-1994;
                                                                                                                                                                                                                                                                                    12-JUL-1990;
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                                                      01-JUN-1999
                                                                                                                                                                                                             22-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Si
Matches 201;
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RESULT 1

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Human lymphotropic virus type III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS; acquired immunodeficiency syndrome; viral infection; env protein; fusion polypeptide; E' protein; gag protein; pol protein; P' protein; gD signal peptide; detection; vaccination; etiological agent; infection inhibitor; AIDS associated retrovirus; p24; gp41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
                                                                                                                                                                                                                                                              Purified glyco:protein and peptide(s) - are recognised by sera contg. antibodies against lymphadenopathy virus and useful in detecting AIDS antibodies or in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim a polypeptide which is recognised by sera of human origin contg. antibodies against the virus of lymphadenopathies (LAV) or acquired immune deficiency syndrome ATDS). Also claimed are various peptides corresp. to the AA sequences deducible from proteins encoded by LAV DNA, defined by specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance with a formula given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                     Montagnier L, Krust B, Chamaret S, Clavel F, Chermann J-C;
Barre-Sinoussi F, Alizon M, Sonigo P, Stewart C, Danos O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 48.9%; Score 1107; DB 7; Length 216; Local Similarity 98.1%; Pred. No. 2.7e-96; less 202; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90179 standard; Protein; 206
                                                                                                                                CENT NAT RECH SCI
                                                                            85GB-0001473.
                                                                                       84FR-0016013.
84GB-0029099.
                                                  85WO-EP00548
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                                                                                                                                            ) INST PASTEUR
                                                                                                                                                                                                                         WPI; 1986-119166/18.
N-PSDB; AAN60365.
                                                                                                                                                                                                Wain-Hobson S;
                                                                                                                                (CNRS ) CNRS
                                                                                          18-OCT-1984;
16-NOV-1984;
                                                  18-OCT-1985;
                                                                            21-JAN-1985;
WO8602383-A
                       24-APR-1986
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Matches
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This invention describes a novel fusion polypeptide which comprises (a) a first polypeptide sequence of an AIDS associated E', env, or gap polypeptide, that specifically binds complementary antibody and (b) a second polypeptide sequence which is not an AIDS associated virus polypeptide. Also described are are (1) a fusion polypeptide having a herpes simplex virus (HSV) gD signal peptide sequence fused in reading frame with a polypeptide sequence other than HSV gD, (2) a nucleic acid encoding a fusion polypeptide as in (1); (3) an expression vector comprising a nucleic acid as in (2); (4) a host comprising a vector as in (3). The AIDS-associated fusion polypeptides can be used in the detection of and vaccination against viral etiological agents of AIDS. They can also be administered as a pharmaceutical agent to inhibit infection by AIDS associated retrovirus or dissemination of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New AIDS-associated fusion poly:peptide(s) - used for the detection of AIDS or to inhibit infection by AIDS associated retrovirus or dissemination of such retrovirus in infected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 2A-J; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrovirus in infected individuals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840S-0685272
85US-0805069.
88US-0227568.
92US-0979391.
93US-0129009.
                            /label - Val,
                                                                               'label Thr,
                                                                                                                                    /label- Asp,
                                                                                                                                                                                       label- Glu,
                                                                                                                                                                                                                                             'label- Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0861016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0282857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capon DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-094894/08.
                                                                                                                                                                                                                                                                         Misc-difference 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 198; Conser
                                                                                                                                                              Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV74271
Misc-difference
                                                     Misc-difference
                                                                                                        Misc-difference
                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1988;
19-NOY-1992;
                                                                                                                                                                                                                                                                                                                                                        JS5853978-A
                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berman PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 - DEC - 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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the procession vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral conservation in infected individuals and/or for reducing transmission rate to previously uninfected individuals and/or for reducing levels of viral or lower with the present sequence is human immunodeficiency virus-1 (HIV-1) iffl Nef protein. The different codon optimised nef constructs of the invention are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                       DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; mutant; mutein.
               291
FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a DNA vaccine comprising a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2
                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1
                                                                             LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                             Ą
                                                                                                                                                                          AAE04960 standard; Protein; 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 13; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2000; 2000WO-US34162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0172442
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                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                          HIV-1 jrfl Nef protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiver JW, Llang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-417878/44.
N-PSDB; AAD09603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200143693-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1999;
                                                                                                                                                                                                                                          10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nvention
                                                                                                                                                                                                            AAE04960;
                                                            292
                                                                                            181
                                                                                                                                                            AAE04960
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Length 216;

DB 22;

44.7%; Score 1011;

Query Match

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This sequence represents a protein of unspecified function contained in a complete nucleotide sequence of ARV-2 derived from partial sequences of several ARV clones. The invention provides a method for construction of a vector for expression of a polypeptide in a mammalian cell, comprising a polypeptide coding sequence operably linked downstream of an enhanced promoter. The enhanced promoter comprises the human cytomegalovirus immediate early region (HGW IEL) promoter. The polypeptide can be any of the HIV recombinant polypeptides and especially HIV gpl20. Expression of HIV gpl20 by COS 7 cells transfected with pCMV6a containing the gpl20 coding region, where pCMV6a is a vector containing the above enhanced promoter,
                                                                                                          ------GVGAASRDLEKHGAITSSNTAA 161
                                                                                                                                                 DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 281
              Gaps
                                                                   1 mggkwskrsvpgwstvrermrraepaadrvrrtepaavgvgavsrdlekhgaitssntaa 60

    comprising cytomegalovirus

                                                                                              TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL
              10;
                                                                                                                                                                                                                                                                                                                                                                                     Protein 6 contained in a complete ARV-2 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                enhanced promoter; gene expression; cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenberg
              Indels
ed. No. 3.2e-87;
Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luciw PA,
                                                                                                                                                                                                                     282 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enhanced promoter for gene expression immediate early promoter plus intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4C-P; 99pp; English
                                                                                                                                                                                                                                                                                                       Ä
                                       MGGKWSKSSVVGWPTVRERMRRAEPAAD-
                                                                                                                                                                                                                                                                                                    AAW53113 standard; Protein; 210
Similarity 83.8%; Pre
31; Conservative 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85US-0773447.
92US-0931191.
93US-0083391.
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94US-0288336
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85US-0696534
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chapman BS, Dina D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-007982/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                          25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5688688-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1993
 Best Local Sim
Matches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thayer RM;
                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                AAW53113;
                                                                                                                                                                                                                                                                                                                                                                                                                ARV-2;
                                         112
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N-PSDB; AAD09605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1999;
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                                                           CRL 8597).
                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                AAE04962;
                                                                             Sequence
                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                121
                                                                                                                                                                             168
                                                                                                                                                                                                                                                  288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the improvement of HIV-1 immunoassays by the use of an HIV-1 antigen comprising an immunogenic fragment of recombinant or synthetic HIV-1 pol, which is encoded by an approximately 9.7 kb sequence between a BstXI restriction site at position 3006 and an Ndel site at position 5131 of the genome (the proviral DNA sequence is
                                                                                                                                                                                                                                                                                                                               HIV-1; immunoassay; antigen; pol fragment; p31; recombinant; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y for antibodies against human immune deficiency virus, for infection, uses an immunogenic fragment of the pol protein
                                                                                                                                 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 167
                                                                                                                        168 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 227
                                                                                                                                                            287
                                                                     Gaps
is increased by a factor of 50 \cdot 100 compared with the use of a vector containing the 5 v 40 early promoter.
                                                                                                TOGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                   Length 210;
                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 'ATCC CRL 8597'
                                                  ; Score 997; DB 19;
; Pred. No. 6.4e-86;
16; Mismatches 11;
                                                                                                                                                                                                                                                                                                               HIV-1 (ATCC CRL 8597) ORF #3-encoded protein.
                                                                                                                                                                                              Example 1; Fig 40-P; 99pp; English.
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                                                                                                                                                                                                                                                          AAY77299 standard; Protein; 210
                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0089407.
87US-0138894.
92US-0931154.
84US-0667501.
85US-0696534.
85US-0773447.
                                                   44.0%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                              95US-0443434
                                                                                                                                                                                                                                                                                             (first entry)
                                                            Best_Local Similarity 85.29
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-170256/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dina D;
                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-170256/
N-PSDB; AAZ90201
                          210
                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoassay
                                                                                                                                                                                                                                                                                             22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                          US6013432-A.
                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000
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17-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing
as antigen
                                                                                                                                                                                                                                                                                                                                           detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luciw PA,
                                                                                                                                                                                                                                                                           AAY77299;
                           Sequence
                                                    Query Match
                                                                                      112
                                                                                                                                          61
                                                                                                                                                            228
                                                                                                                                                                                               288
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                                                                                                                                                                                                                                                  AAY77299
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given in AAZ90201). The immunogenic pol fragment is not immunologically. Cross- reactive with human T cell lymphotropic viruses I or II. The invention also encompasses the used of p31 as an antigen. The recombinant antigens may be produced in Escherichia coli, Saccharomyces cerevisiae or in mammalian cells. Immunoassays using the recombinant HIV proteins may be used to diagnose and stage HIV-1 infections. Sequences AAY77294-Y77299 represent proteins encoded by the genome of HIV-1 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type myristylation site at Gly2 substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "Wild type dileucine motif (Leu-Leu) substituted
with Ala-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; jrfl Nef; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 227
                                                                                                                                                                                                                                                                                                                                                                                                     112 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                 TQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                                                                                                                                                                                                                                                                                                                         .,
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                                                                                                                                                                                                                                                                                                  Length 210;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                     Score 997; DB 21;
Pred. No. 6.4e-86;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1 jrfl Nef (G2A, LLAA) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE04962 standard; Protein; 217
                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                     44.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with Ala"
174..175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-417878/44.
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 179; Conserv
                                                                                                                                                                                                                               210 AA;
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Purified human retrovirus - is mutant of HIV-1 having characteristics of HIV-1 OYI, used in diagnosis of HIV infection

WPI; 1991-177518/24

Disclosure; fig 8; 23pp; English.

us-09-509-239-21.rag

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capression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for Inducing a cell mediated immune (cytcoxic T lymphocyte, CTL) response against infection or disease cused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human immunodeficiency virus-1 (HIV-1) jifil Nef (G2A, LLAA) mutant protein. The different nef constructs of the invention are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA
                                                                                                                                                                   present invention relates to a DNA vaccine comprising a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 22;
8.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%; Score 996; 82.0%; Pred. No. 8
                                                                                                                      Page 18; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AA
                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                    Claim
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TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 221
                                               DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 281
                                                       9
HIV-1 strain OYI open reading frame (ORF) F protein.
                                                                           HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNCT 318
                                                                                  A
                                                                                                                            AAR12262 standard; Protein; 210
                                                                                                                                                                                                                                              87US-0113655
                                                                                                                                                                                                                                                            87US-0113655
                                                                                                                                                         (first entry)
                                                                                                                                                                                     HIV-1; AIDS;
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                             28-OCT-1987;
                                                                                                                                                                                                                                                            28-OCT-1987;
                                                                                                                                                         20-AUG-1991
                                                                                                                                                                                                                 US5019510-A.
                                                                                                                                                                                                                                28-MAY-1991
                                                                                                                                          AAR12262;
                  162
                                                                                         181
                                               222
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                                                                                                                      AAR12262
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                                                                                                                                                                                                                          Gaps
                                                                                         This sequence constitutes the ORF F protein constituent of a new strain of HIV-1 retrovirus, OYI. This mutant retroviral strain is useful in an assay for diagnosing HIV infection. See also AAQ11943 (OXI nucleotide sequence), AAR12255-61 (other HIV OYI constituent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tPA leader peptide-HIV-1 jrfl Nef (opt tpanef) mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-Hi cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; human; jrfl Nef; opt tpanef; tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                          167 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY
                                                                                                                                                                                                                                                                                                                                            HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.26
/label= Leader_peptide
/note= "Human tissue plasminogen activator (tPA)
leader_sequence"
                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                   Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Mature HIV-1 Nef (6-216aa) protein"
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                         6
                                                                                                                                                                                                  Score 983; DB 12;
Pred. No. 1.3e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Human immunodeficiency virus type 1. - Homo sapiens.
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         287 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                     195..196
/label- Dileucine_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                              43.4%; Scor
82.5%; Pref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04961 standard; Protein; 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                              Local Similarity
                                                                                                                                                               210 AA;
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                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-2001
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Chimeric
                                                                                                                                          proteins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE04961;
                                                                                                                                                               Sequence
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Peptide
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99US-0172442

17-DEC-1999;

Brun-Vezinet

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Wain-Hobson

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                                                                                                                                                                                                                                                                The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferrably human. It is also useful for lowering transmission rate to previously uninfected individual, so as to prolong the asymptomatic loads within an infected individual, so as to prolong the asymptomatic activator (tPA) leader peptide-human immunodeficiency virus-1 (HIV-1) irfl Nef (opt tpanef) chimaric mutant protein. The mutation include deletion of the myristylation site (Gly2) in the HIV-1 jifl Nef protein. The different codon optimised nef constructs of the invention are used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; human; jrfl nef; opt tpanef; tissue plasminogen activator; tPA; chimeric protein; mutant; mutein.
                                                                                                                                            Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 SKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAATNAAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIGGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.2%; Score 978; DB 22; Length 237; 83.4%; Pred. No. 4.8e-84; tive 15; Mismatches 10; Indels 10
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                                                                                                                                                                                                                                         Claim 29; Page 17; 84pp; English.
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Matches 176; Conservative
                  (MERI ) MERCK & CO INC.
                                                        Shiver JW, Liang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                         WPI; 2001-417878/44.
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                                                                                                            N-PSDB; AAD09604
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Misc-difference 1957. 196 Misc-difference 1957. 196 Mith Ala-Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
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/label- Leader_peptide
/note- "Human tissue plasminogen activator (tPA)
leader_sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a DNA vaccine comprising a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 237;
                                                                                                               27..237
/note= "Mature HIV-1 Nef (6-216aa) protein"
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82.5%; Pred. No. 4.2e-83;
live 15; Mismatches 12;
Human immunodeficiency virus type 1. Homo sapiens.
                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 29; Page 19; 84pp; English.
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                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                               Liang X,
                                                                                                                                                                                                                                                                                                                                                                           WPI: 2001-417878/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD09606
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                                                                                                                                                                                                                                                                                      17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                               Shiver JW,
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  Chimeric
Chimeric
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                                              Key
Peptide
                                                                                                                  Protein
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ò g antiviral;

cellular immune response; vaccine; treatment; gene therapy.

Human immunodeficiency virus type 1.

/note= "Xaa represents a stop codon

Location/Qualifiers 1..3025 /label xaa

Misc-difference

DE10056747-A1

31-MAY-2001

human; humoral immune response;

HIV-1 subtype C protein fragment #1.

Infection; diagnosis;

(first entry)

21-AUG-2001

standard; Protein; 3025 AA.

AAB86169 AAB86169

AAB86169

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for a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                               human immunodeficiency virus; non-subtype B; gag; pol; env;
lf; vpr; tat; rev; nef; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel genomic nucleic acids of non-subtype B human immunodeficie virus type 1 useful for detecting and treating AIDS comprises a specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                           HIV-1 non-subtype B clone 962M651-8 nef protein.
287 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                            Human immunodeficiency virus type 1.
                                                                                                                                                                                         AAB69363 standard; Protein; 206 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0184418
                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               vpn; vif; vpr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200026416-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1999;
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                                                                                                                                                                                                                                                   AAB69363
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                                         This invention describes a novel polynuclectide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the polypeptides (il) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus 1 (HIV-1) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence in represents a procedule by the HIV-1 subtype C genome described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2723 mggkwsksslvgwpairermrrtepaadgvgavsrdlekhgaltsshtaatnedcawlea 2782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%; Score 948.5; DB 22; 70.6%; Pred. No. 1.2e-79; ... Wiematches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Mismatches
Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                 the method of the invention.
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Best Local S
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Length 206; Indels

Score 952; DB 21; Pred. No. 1.1e-81;

42.0%; 81.1%;

Query Match
Best Local Similarity 81.1
Matches 167; Conservative

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MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171

QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY à

LEWRFDSRLAFHHVARELHPEYFKNC 317 

292 181

g à

FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV

New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of

infection

New

(GENE-) GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG

(SHAO/) SHAO Y.

16-NOV-2000; 2000DE-1056747.

99DE-1055089

16-NOV-1999;

Graf M;

Shao Y,

Wagner R, Wolf H, WPI; 2001-336417/ N-PSDB; AAH20870.

2001-336417/36

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345 CKKCCFHC 352

|: | | 2961 ykgllfac 2968 ò qq

Search completed: August 26, 2002, 08:12:30 Job time: 239 sec

trans-activating t ref protein - bimi nef protein - bimi nef protein - buma trans-activating t nef protein - simi nef protein - simi nef protein - huma nef protein - huma nef protein - huma nef protein - huma nef protein - huma nef protein - buma transactivator pro nef protein - simi transactivator pro tat protein - simi trat protein - simi

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C.Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
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A; Residues: 1-206 < MAIN
A; Residues: 1-206 < MAIN
A; Cross-references: GB: K02013; NID: g326417; PIDN: AAB59752.1; PID: g326425
A; Experimental source: isolate LAV-la
R; Ciccarelli, R.B.
Submitted to the EMBL Data Library, March 1991
A; Reference number: $14607
A; Accession: $14609
A; Status: preliminary
A; Molecule type: DNA
A; Control of the CMBL
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A;Cross-references: EMBL:X58780; NID:g60113; PIDN:CAA41585.1; PID:g60114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nef protein - human immunodeficiency virus type 1 (isolate LAV-la)
N/Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: Actions S14609
R; Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, Cell 40, 9-17, 1985
A; Title: Nucleotide sequence of the AIDS virus, LAV.
A; Reference number: A90866; MUID:85099333
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Pred. No. 2.2e-80;
0; Mismatches 0;
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C;Keywords: AIDS; immunodeficiency; phosphoprotein
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- 2000 Compugen Ltd.
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immune reactivity
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NyAlternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: A04006
C:Accession: A04006
A:Rithe: Three novel genes of human T-lymphotropic virus type III: immune re
A:Reference number: A94093; MUID:86177573
                                                                                                                                                                                        nef protein - human immunodeficiency virus type 1 (isolate LV)
N'Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A04007
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121 FPDXQNYTPGPGVRYPLTFGWCYKLVPVEPDKIEEANKGENTSLLHPVSLHGMDDPEREV 180
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Nature 313, 450-458, 1985
A; Title: Nucleic acid structure and expression of the
A; Reference number: A93355; MUID:85111157
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Pred. No. 1.1e-78;
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Pred. No. 3.9e-79;
3; Mismatches 2;
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                                                                 292 LEWRFDSRLAFHHVARELHPEYFKNC
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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C; Superfamily: AIDS nef protein
C; Keywords: AIDS; immunodeficiency
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97.18;
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ilarity 97.6%;
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Best Local Similarity
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Best Local Simi
Matches 201;
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R; Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
R; Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
Bur. J. Blochem. 221, 811-819, 1994
A; Title: Stability and proteolytic domains of Nef protein from human immunodeficiency via Reference number: S43467; MUID: 94229079
A; Accession: S44467
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-205 < FRE>
C; Superfamily: AIDS nef protein
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N.Alternate names: 3'-orf protein
N.Alternate names: 3'-orf protein
C.Species: human immunodeficiency virus type 1, HIV-1
C.Species: Luman immunodeficiency virus type 1, HIV-1
C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
C.Accession: 503244
R.Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa Nucleic Acids Res. 13, 8219-8229, 1985
A.Title: Polymorphism of the 3' open reading frame of the virus associated with the acquare A.Reference number: 503244; MUID:86067228
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                                           nef protein – human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
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                                                                                                                                                                                                                                                                                                                                                              Score 1115; DB 2;
Pred. No. 3.2e-79;
0; Mismatches 2;
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Pred. No. 3.3e-79;
2; Mismatches 1;
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A.Molecule type: DNA
A.Residues: 1.206 <RAT>
A.Cross-references: EMBL:X03187
A.Mote: the in-frame stop codon at
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Best Local Similarity 98.5%;
Matches 203; Conservative
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Best Local Similarity 99.0%;
Matches 203; Conservative
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Gene: nef; 3'-orf; orf-F
Superfamily: AIDS nef protein
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Gaps

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nef protein - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1,
C; Species: human immunodeficiency virus type 1,
C; Species: human immunodeficiency virus type 1,
C; Species: human immunodeficiency virus type 1,
C; Species: S33986
B; Carlini, F.
Submitted to the EMBL Data Library, November 1991
A; Reference number: S33979
A; Recession: S33986
A; Status: preliminary
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                                                                                                                                                                                                    NID:960192; PIDN:CAA77629.1; PID:960200
A;Cross-references: EMBL:X03188; NID:g61556; PIDN:CAA26947.1; PID:g61557
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Pred. No. 9.7e-78;
                                                                                                          Score 1096; DB 2;
Pred. No. 9.7e-78;
4; Mismatches 3;
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3; Mismatches
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96.68;
                                                                                                          48.4%;
96.6%;
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A) Cross-references: EMBL:211530;
C) Superfamily: AIDS nef protein
               C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
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                                                                                                                                             Conservative
                                                                                                          Query Match
Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Matches 199;
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503245

nef protein (clone HXB3) - human immunodeficiency virus type 1
N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus 20-Sep-1999
C;Accession: S03245
A;Reference number: S03244; MUID:86067228
A;Reference number: S03344
A;Residues: 1-206 <RAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part possesses membrane-perturbing and fusogenic activitie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to yeast
                                                                                                                                                                                                                                                                                                                                                                   uer protein - Human immunodeficiency virus type 1, HIV-1
C; Species: Human immunodeficiency virus type 1, HIV-1
C; Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 31-Oct-1997
C; Accession: JC5400
R; Macreadie, I.G; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.
Blochem. Blophys. Res. Commun. 232, 707-711, 1997
A; Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to A; Reference number: JC5400; MUID:972/1389
A; Accession: JC5400; MUID:972/1389
A; Accession: JC5400; MUID:972/1389
A; Accession: JC5400
A; Readdues: 1-206 < AGC>
C; Comment: The amino-terminal part possesses membrane-perturbing and fusogenic accistors and by the content of protein #status results.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
                                  MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                       QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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2; Indels
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Pred. No. 8.1e-78;
1; Mismatches 5;
Mismatches
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ilarity 97.1%;
Conservative
Conservative
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Best Local Simi
Matches 200;
200;
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 Matches
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Gaps

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us-09-509-239-21.rpr

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A;Cross-references: GB:M21098; NID:g326426; PIDN:AAA44222.1; PID:g326431
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detailed to number: S21990
A;Reference number: S21993
                                                                                                                                                                                                                                    A; Note: host Homo sapiens (man)
C; Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jul-1999
C; Cecession: D31667; S21993; S21995; S21999; S21999; S21991; S21991; S21991; S21993; S21995; S21991; S21991; S21993; S21995; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S21991; S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43625.1; PID:g1129140; EMBL:X61
A:Accession: S21999
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 25-Feb-1994 #sequence_revision 01-bec-1995 #text_change 20-Sep-1999
C;Accession: S25937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-7 <ST2>
A;Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43623.1; PID:g584028;
A;Accession: S21997
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                                                                                                                          nef protein - human immunodeficiency virus type 1 (isolate N;Alternate names: 3'-orf protein; orf-F protein C;Species: human immunodeficiency virus type 1, HIV-1
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84.1%; Pred. No. 9.9e-72;
live 12; Mismatches 7;
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Nature 349, 745-746, 1991
A;Title: Sequence analysis of original HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 MGGKWSKSSVVGWPTVRERMR----
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Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 185; Conserv
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A; Residues: 1-7 <ST3>
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A; Residues: 1-7 <ST4>
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A; Accession: S21995
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submitted to the EMBL Data Library, November 1991
A; Description: In vivo derived HIV-1 NEF genes are heterogeneous and lack detectable a; Reference number: S24985
A; Accession: S24985
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-204
A; Chara-A, A; Chara-A, A, Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; Chara-A, A; 
    .; Josephs, S.F.;
Wong-Staal, F.
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Sep-1999
C;Accession: S24985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 MGGKWSKSSVVGWPTVRERMRREPPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wo Nature 313, 277-284, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 205;
                                                                                                              A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123
A:Reference number: A93353; MUID:85111123
A:Accession: A04005
A:Molecule type: DNA
A:Residues: 1-205 <RAT>
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS: immunodeficiency
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Pred. No. 1.3e-76;
4; Mismatches 3;
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Best Local Similarity 89.8
Matches 185; Conservative
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ses 198; Conserv
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Best Local S
Matches 198
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PID:9584027; EMBL:X613

EMBL: X613

Gaps

16;

Length 218; Indels

Aug

Mon

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nef protein - human immunodeficiency virus type 1 (strain YU-2)

N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo saptens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Feb-1997
C;Accession: I44001
R;Li, Y; Hui, H; Burgess, C.J; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J, Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties
                                                                                                                                                                                                                                                                             A, Accession: 144001
A, Molecule type: DNA
A, Residues: 1-214 <LIV3
A, Cross references: GB:M93258
C; Genetics: 3'-orf; orf-F
C; Superfamily: AlDS nef protein
C; Keywords: AlDS; immunodeficiency
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Best Local Similarity 98.4%;
Matches 179; Conservative
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Matches 18
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N.Alternate names: 3'-orf protein; orf-F protein
N.Alternate names: 3'-orf protein; orf-F protein
A.Alternate names: 3'-orf protein; orf-F protein
A.Alternate names: 3'-orf protein; orf-F protein
A.Alternate names: 1'-way-1885 #sequence_revision 1'-may-1985 #text_change 16-Jul-1999
C.Date: 17-Way-1885 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C.Date: 17-Way-1885 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C.Date: 17-Way-1885 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R.Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh-Aritie: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A.Accession: A04009
A.A.Accession: A04009
A.Molecule type: DNA
A.Residues: 1-210 <SAN>
A.Gross-references: GB:K02007; NID:9328658; PIDN:AAB59883.1; PID:9328667
A.Genetics: A.Gene: nef; A.A.D.S. nef protein
A;Reference number: S25937; MUID:91156044
A;Accession: S25937
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: nucleic acid
A;Residues: 1-206 <GUO>
A;Cross-references: EMBL:X57465; NID:960217; PIDN:CAA40702.1; PID:960218
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C;Superfamily: AIDS nef protein
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4
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                                                                                                                                                                                                              Query Match
44.5%; Score 1007; DB 2;
Best Local Similarity 85.9%; Pred. No. 7.9e-71;
Matches 177; Conservative 18; Mismatches 11;
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44.0%; Score 997; DB 1;
Best Local Similarity 85.2%; Pred. No. 4.8e-70;
Matches 179; Conservative 16; Mismatches 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: nef; 3'-orf; orf-F; Superfamily: AIDS nef protein; Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                172
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Ritation, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pett Nucleic Acids Res. 13, 8219-8229, 1985
A; Fitle: Polymorphism of the 3' open reading frame of the virus associated with the a A; Accession: S03244; MUID:86067228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nef protein (clone C15) - human immunodeficiency virus type 1 (fragment) N'Alternate names: 3'-orf protein C;Species: human immunodeficiency virus type 1, HIV-1 C;Bate: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Jun-2000 C;Accession: S03247
                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-182 <RAT>
A;Cross-references: EMBL:X03189; NID:961552; PIDN:CAA26948.1; PID:91335562
                                                                                                                                                                                                                                                                                                                      112 MGGKWSKSSVVGWPTVR-----ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA 161
                                                                                                                                                                                                 162 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 221
                                                                                                                                                                                                                                                                                               DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 PAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAA 195
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  Length 214;
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                                                     Indels
43.8%; Score 991.5; DB 1;
84.2%; Pred. No. 1.3e-69;
iive 12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 987; DB 2;
Pred. No. 2.4e-69;
1; Mismatches 2.
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C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999 C; Accession: J00068 F; Spirer, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, Gene 81, 275-284, 1989 A; Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human im A; Reference number: J00065; MUD: 90034200 A; Accession: J00068 A; Molecule type: DNA A; Residues: 1-207 <SPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nef protein - human immunodeficiency virus type 1 (isolate 2321)
N'Alternate names: 3'-orf protein, orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 *sequence_revision 17-Feb-1994 *text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QEESEEVGFPVRPQVPLRPMTYKEAVDLSHFLKEKGGLEGLIMSKRQEILDLWVYNTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDFERE 290
                                                                                                                                                                    112 MGGKWSKSSVVGWPTVRERM-----RRAEPAADGVGAASRDLEKHGAITSSNTAATNAAC 166
                                                                                                                                                                                                                                                                                  167 AWLEAQEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWI 225
                                                                                                                                                                                                                                                                                                               YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD 285
                                                                                                                                                                                                                                                                                                                                                                                                                             112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                                                                                                                   Gaps
                                                                                                                                                                                                    A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA4874.1; PID:g328163
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG
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                                                               Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nef protein - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
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                                                                                                     19; Indels
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Pred. No. 8.6e-63;
                                                         Score 911; DB 1;
Pred. No. 2.3e-63;
; Mismatches 19.
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77.3%; Pred. No. o...
'... 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 DPEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
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                                                                                                                23;
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C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
                                                         40.2%;
ilarity 77.4%;
Conservative 2
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Matches 160;
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Matches 164;
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                                                                                                                                                                                                                                                                                                                                                          The protein (clone HAT3) - human immunodeficiency virus type 1
N.Alternate names: 3'-orf protein
N.Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Accession: S03246
R;Ratner L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettewa Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu A;Accession: S03246
A;Accession: S03246
A;Residues: 1-204 <RAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X03190; NID:g61550; PIDN:CAA26849.1; PID:g61551 A;Note: the authors translated the codon AGT for residue 11 as Gly C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFHVARELHPEYFK
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NC 182
                                                                                                                                                                                           316 NC 317
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- Haemophilus influenzae (strai
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Def protein - simian immunodeficiency virus SIVopz

NiAlternate names: 3'-orf protein; orf-F protein

C.Species: simian immunodeficiency virus SIVopz

A:Note: host Pan troglodytes (chimpanzee)

C.Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C.Saccession: S09991

R:Huet, T.: Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 356-359, 1990

A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A:Reference number: S09983; MUID:90259077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S09991
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-205 <HUE>
A;Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36408.1; PID:958877
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-364 <SON>
A;Residues: 1-364 <SON>
A;Cross-references: BYBL:235656; NID:g52213; PIDN:CAA84715.1; PID:g526
A;Experimental source: strain 3639
C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
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46.9%; Pred. No. 1.4e-36;
live 19; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 832; DB 1; Pred. No. 3e-57; 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 LEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Gene: nef
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency
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Best Local Similarity 46.9°
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144; Conservative
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Best Local Similarity
Matches 144; Conserv
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: T01673
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
R;Accession: T01673
R;Reference number: Z14389; MUD:86245056
R;Reference number: Z14389; MUD:86245056
R;Reference number: L10873
R;Reference number: L10873
R;Residues: 1-209 - ALIS
R;Residues: 1-209 - ALIS
R;Cross-references: EMBL;R03456; NID:960228; PIDN:CAA28017.1; PID:960235
C;Superfamily: AlDS nef protein
                                                                                                                    2
C; Accession: B44963
R; Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, AIOS Res. Hum. Retrovivruses 5, 121-129, 1989
A.Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: A; Reference number: A44963; MUID:89228766
A; Accession: B44963
A; Molecule type: DNA
A; Molecule type: DNA
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70.1%; Pred. No. 2e-57;
1ve 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.0%; Score 837; DB 1;
73.2%; Pred. No. 1.2e-57;
iive 23; Mismatches 25
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Best Local Similarity 70.1%;
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 73.28
Matches 153; Conservative
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"Alternate names: immunoglobulin D-binding protein; protein D
N; Alternate names: immunoglobulin D-binding protein; protein D
C; Species: Haemophilus influenzae
A; Variety: isolate 772
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-oct-1999
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-oct-1999
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-oct-1999
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-oct-1999
C; Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-oct-1999
R; Janson, H.: Heden, L.O.: Grubb, A.: Ruan, M.: Forsgren, A.
A; Title: Protein D, an immunoglobulin D-binding protein of Haemophilus Influenzae: Clay Molecule type: DNA
A; Reference number: A43576
A; Molecule type: DNA
A; Residues: 1-364 < JANA
A; Residues: 1-364 < JANA
A; Residues: 1-364 < JANA
A; Experimental source: Isolate 772
C; Keywords: lipoprotein; phosphoric diester hydrolase; |surface antigen F; 1-18/Domain: signal sequence #status predicted <SiG>C; Keywords: lipoprotein; phosphodiester phosphodiesterase #status predicted <MAT>F; 19-364/Product: glycerophosphodiester phosphodiesterase #status predicted <MAT>
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C. Species: Haemophilus influenzae

A:Variety: strain Eagan; strain HK695

C:Accession: S59934; S59935; S47336; S47337

C:Accession: S59934; S59935; S47336; S47337

R:Song, X.M.; Forsgren, A.; Janson, H.

Infect. Immun. 63, 696-699, 1995

A:Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus inf. A:Reference number: S59931; MUID:95122210

A:Reference number: S59931; MUID:95122210
               - Haemophilus influen
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A;Cross-references: BMBL:235660; NID:9525221; PIDN:CAA84719.1; PID:9525222
A;Experimental source: strain HK695
C;Reywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIHSQRRQDILDLWIYHTQGYFPDWQ-----NYTPGPGVRYPLTFGWCYKLVPVE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL;235659; NID:9525219; PIDN:CAA84718.1; PID:9525220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 ---ETQEKDPKGYWV----NYNYDWMFKPGAMAEVVKYADGVGP'-----GW-YMLVNKE 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 HGAITSSNTAATNAACAMLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.2%; Score 569.5; DB 2 46.9%; Pred. No. 1.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental, source: strain Eagan
A, Accession: S59935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 144; Conserv
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A; Residues: 1-364 <SON>
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otein D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenz N:Alternate names: Immunoglobulin D-binding protein; protein D C;Species: Heamophilus influenzae A:Varlety: strain 3640 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999 C;Song, X.M.; Forsgren, A.; Janson, H. Infect. Immun. 63, 696-699, 1995 A;Title: The gene encoding protein D (hpd) is highly conserved among Haemoph A;Reference number: S$9931; MUID:95122210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-364 <SON>
A;Cross-references: EMBL:235657; NID:9525215; PIDN:CAA84716.1; PID:9525216
A;Experimental source: strain 3640
C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150
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                                                                                                                                                                                                                                                                                                                                                   211 LIHSQRRQDILDLWIYHTQGYFPDWQ------NYTPGPGVRYPLTFGWCYKLVPVE 260
                                                                                                                                               --SKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 FPLWKSHFRIHTFEDEIEFIQGLEKSTGKKVGIYPEIKAPWFHQNGKDIAAETLKVLKK 199
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                                                                          151 HGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG
                                                                                                                                                                                                                                                                                                   200 YGYDKKTD------MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK----
SSHSSNWANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
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                                               64 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGK-
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46.9%; Pred. No. 1.4e-36;
Live 19; Mismatches 71;
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Matches 144; Conservative
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ESKPDNI 299
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RESULT

us-09-509-239-21.rpr

F;1-18/Domain: signal sequence #status predicted <sig> F;19-364/Product: protein D #status predicted <mat></mat></sig>	QY 211 LIHSQRRQDILDLWIYHTGGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVE 260  1
Query Match 25.2%; Score 569.5; DB 2; Length 364; Best Local Similarity 46.9%; Pred. No. 1.4e-36; Matches 144; Conservative 19; Mismatches 71; Indels 73; Gaps 11;	Oy 261 PDKV 264  Db 293 ESKPDNI 299
OY 4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 63	RESULT 27
VIHDHFLDGLTDVAKKPPHRHRKDGRYYVIDFTLKEIOSLEMTENFETMGGK IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strai N.Alternate names: IgD-binding protein; protein D C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text, change 21-Jul-2000
QY 116WSKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150  DD 140 FPLWKSHFRIHTFEDEIEFIGGLEKSTGKKVGIYPEIKAPWFHHQNGKDIAAETLKVLKK 199	Tames, M.D.; White, O.; Clayton, R.A.; Kirk J.; Shirley, R.; Liu, L.I.; Glodek, A.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.
OY 151 HGAITSSNTAATNAACAWLEAQEEEFVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG 210 1	Solence 209, 495-312, 1955 A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A.71itle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630
OY 211 LIHSORRODILDLMIYHTQGYFPDWQNYTPQGVRYPLTFGWGYKLVPVE 260  247ETQEKDPKGYWVNYNYDWMFKPGAMAEVVKYADGVGPGW-YMLVNKE 292	translation not shown
Oy 261PDKV 264  Db 293 ESKPDNI 299	A):Toss references: us:002/31; us:442023; NID:93114200; FIDN:4AC21348.1; FID:915/3590 A):Experimental source: strain Rd KW20 C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
RESULT 26 S59933 91Ycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strain 6	Query Match 24.4%; Score 553.5; DB 2; Length 364; Best Local Similarity 45.9%; Pred. No. 2.5e-35; Matches 141; Conservative 21; Mismatches 72; Indels 73; Gaps 11;
N.Alternate names: immunoglobulin D-binding protein; protein D C;Species: Haemophilus influenzae A;Variety: strain 6-7626 C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 08-0ct-1999	QY 4 SSHSSNMANTOMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 63  20 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQHSDYLEQDLAMTKDGRLV 79
	QY 64 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMFETMGGK 115
3	OY 116W
A.Cross-references: EMBL: 235658; NID:9525217; PIDN:CAA84717.1; PID:9525218 A.Experimental source: strain 6-7626 C.Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen	QY 151 HGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVLLSHFLKEKGGLEG 210  1 :
Query Match  24.9%; Score 563.5; DB 2; Length 364;  Best Local Similarity 46.6%; Pred. No. 4.2e-36;  Matches 143; Conservative 19; Mismatches 72; Indels 73; Gaps 11;	QY 211 LIHSQRRQDILDLWIXHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVE 260  DD 247ETQEKDPKGYWVNYNYDWMFKPGAMAEVVKYADGVGPGW-YMLVNKE 292
OY 4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 63	Qy 261PDKV 264  Db 293 ESKPDNI 299
Qy 64 VIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGK 115	RESULT 28 S59936 glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Haemophilus influenzae (strai
QY 116WSKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150  DD 140 FPLWQSHFRIHTFEDEIEFIGGLEKSTGRKVGIYPEIKAPWFHHQNGKDIAAETLKVLKK 199	N.Alternate names: IgD-binding protein; protein D C.Species: Haemophilus influenzae A.Variety: strain NCTC 8468 C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
Qy 151 HGAITSSNTAATNAACAWLEAQEEEUGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG 210	C; Accession: S5935; S47338 R:Song, X.M.; Forsgren, A.; Janson, H. Infect. Immun. 63, 696-699, 1995 A.Title: The gene encoding protein D (hpd) is highly conserved among Haemophilus infl A; Reference number: S59931; MUID:95122210

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August 26, 2002, 08:13:23
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A;Residues: 1-95 <ARY>
C;Genetics:
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Job time: 292 sec
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A; Residues: 1-86 <CARS
A; Cross-references: 1-86 <CARS
A; Cross-references: BEBL:211530; NID:960192; PIDN:CAA77625.1; PID:960196
B; Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Sumner-Sm
Nucleic Acids Res. 20, 5311-5320, 1992
Nucleic Acids Res. 20, 5311-5320, 1992
A; Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator of
A; Reference number: S26385; MUID:93065196
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A;Accession: S59936
A;Rolecule: 1-364 - SONS-
A;Residues: 1-364 - SONS-
A;Cross-references: EMBL:235661; NID:9525223; PIDN:CAA84720.1; PID:9525224
A;Experimental source: strain NCTC 8468
C;Keywords: lipoprotein; phosphoric diester hydrolase; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 PPLWKSHFRIHTFEDEIEFIQGLEKSTGKKVGIYPEIKAPWFHHQNGKDIAAETLKVLKK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIHSQRRQDILDLWIYHTQGYFPDWQ------NYTPGPGVRYPLTFGWCYKLVPVE 260
                                                                                                                                                                                                                                                                                                                                                                                                              64 VIHDHFLDGLIDVAKKFPHRHRKDGRYYVIDFILKEIQSLEMTENFETMGGK------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                           --SKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                                                                                                                                                                                                                                                                                                                         20 SSHSSSMANTQMKSHKIIIAHRGASGYLPEHTLESKALAFAQHADYLEQDLAMTKDGRLV 79
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                                                                                                                                                                                                                                                                                                            SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: nucleic acid
A; Residues: 1-86 <SID>
A; Cross-references: EMBL:X64650; NID:g60144; PIDN:CAA45921.1; PID:g60145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 YGYDKKTD------MYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK-----
                                                                                                                                                                                                                  Length 364;
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C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                        Ouery Match 24.2%; Score 547.5; DB 2; Best Local Similarity 45.6%; Pred. No. 7.4e-35; Matches 140; Conservative 20; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.5%; Score 486; DB 2; L. Best Local Similarity 100.0%; Pred. No. 7.4e-31; Matches 85; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Carlini, F. submitted to the EMBL Data Library, November 1991 A:Reference number: S33979 A;Accession: S33982
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trans-activating transcription regulator - human immunodeficiency virus type 1 (isol Cispecies: human immunodeficiency virus type 1, HIV-1 A.Note: host Homo sapiens (man) C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.S.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.C.Date: 04-Dec-1986 *text_change 02-Jul-1998 C.S.C.C.C.C.C.C.C.Date: 04-Dec-1986 C.S.C.C.C.Date: 04-Dec-1986 C.S.C.C.Date: 04-Dec-1986 C.S.C.C.C.Date: 04-Dec-1986 C.S.C.C.Date: 04-Dec-1986 C.S.C.C.Date: 04-Dec-1986 C.S.C.C.Date: 04-Dec-1986 C.S.C.C.Date: 04-Dec-
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C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation
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Pred. No. 3.5e-30;
0; Mismatches 1;
380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
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                                                                          SQTHQVSLSKQPTSQSRGDPTGPKE
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98.8%;
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Best Local Similarity 98.8
Matches 84; Conservative
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Sequence 43, Appl Sequence 1, Appl1 Sequence 15, Appl Sequence 15, Appl Sequence 4, Appl Sequence 4, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1, Appl Sequence 1, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TILLE REPERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR PAPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 76
LENGTH: 239
                                                                                                                                                                                                                                    Sequence
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25; Indels
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88.7%; Pred. No. 5e-107;
Live 2; Mismatches 25;
US-08-816-155B-43
US-09-079-587-43
US-09-099-333-1
US-08-047-210A-96
US-08-047-210A-96
US-08-059-256-490-4
PCT-US9-11445-4
US-09-256-490-4
US-09-256-490-4
US-09-451-905-17
US-08-893-853-1
US-08-893-853-1
US-08-893-853-1
US-08-893-853-1
US-08-094-128A-27
US-08-094-128A-27
US-08-455-992-27
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COTHER INFORMATION: X os selenocysteine.
US-08-679-493A-76
                                                                                                                                                                                                                                                                                                                                              Sequence 76, Application US/08679493A Patent No. 6303295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.77
Matches 211; Conservative
  NAME/KEY: VARIANT
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                                                                                          August 26, 2002, 08:10:40; Search time 38.46 Seconds (without-alignments) 262.293 Million cell updates/sec
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2264
1 MDPSSHSSNMANTQMKSDKI.....QSRGDPTGPKETSGHHHHH
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-485-885-8
US-09-485-885-16
US-09-485-885-16
US-09-485-885-6
US-09-485-885-4
US-09-485-885-4
US-09-495-885-4
US-09-455-885-4
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                        Scoring table:
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112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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; Sequence 75, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TILLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REPERENCE: 55-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILNG DATE: US/08/488,551B
FILNG DATE: US/08/488,551B
FILNG DATE: US/08/48,551B
APPLICATION NUMBER: PW3864 (AU)
FILNG DATE: 21-FEB-1994
APPLICATION NUMBER: PW4002 (AU)
FILNG DATE: 21-FEB-1994
APPLICATION NUMBER: PW0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: US 08/388,353
APPLICATION NUMBER: PW3021/95
APPLICATION NUMBER: PW3021/95
  NON-PATHOGENIC STRAINS OF HIV-1
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Pred. No. 8.5e-105;
1; Mismatches 3;
                                                        E: SCULLY, SCOTT, MURPHY & PRESSER 400 GARDEN CITY PLAZA
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                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 644:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.2%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: FRANK S. DIGIGLIO REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.1
Matches 202; Conservative
                                                                                                                      ZIP: 11530-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-488-551B-644
                         NUMBER OF SEQUENCES: 8
                                                           ADDRESSEE: SCULLY
STREET: 400 GARDE
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                   CITY: GAR
STATE: NE
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGGKWSKSSVIGWPAVRERMRRAEPAADGVGAVSRDLEKHGAITSSNTAANNAACAWLEA 60
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                                                        APPLICANT: Deacoo, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Memory Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      ZIP: 11530
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1115; DB 3;
Pred. No. 8.5e-105;
1; Mismatches 3;
                                                                                                                                                                                                                       ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 644, Application US/08488551B Patent No. 6015661
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Sequence 644, Application US/08388353 Patent No. 6010895
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APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: DiG1glio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.1%;
Matches 202; Conservative
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TELEFAX: (516) 742-4366
TELEE: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
                                                                                                                                                                                                                                                                                    New York
: United States
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                                                                                                                                                                                                                                                               Garden City
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STATE:
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235 WONYTPGPGVRYPLTFGWCYKLV-------PVEPDKVEE+ANKGENTSLLHPV 279
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                                                                                                                61 RLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTËNFETMGGKWSKSS 120
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                                        MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                                                              Indels 177;
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      Indels
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36.4%; Pred. No. 6.7e-53;
ive 26; Mismatches 73;
      'n,
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Warie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Benchelkh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR PELICATION NUMBER: PCT/EF98/05285
PRIOR APPLICATION NUMBER: PCT/EF98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1998-08-17
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      Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 278
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    Conservative
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US-09-485-885-21
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Best Local Similarity
Matches 158; Conserv
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                                                                                                                                                                                                                                                                                                                                Sequence 21, Appli-
; Patent No. 6342224
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FPD 123
                                                                                                                                                                                             FPD 234
    120;
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 123;
                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 206;
                                                                                                                                                                                                                                                                                                                                                                   Score 971; DB 4; Length 20
Pred. No. 3e-90;
2; Mismatches 15; Indels
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Pred. No. 6.5e-57;
                                                                                                                                                                                                             ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human imunodeficiency virus type
CURRENT.APPLICATION NUMBER: US/08/679,493A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVLEWRFDSRLAFHHVARELHPEYFKNC 317
  CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: 60/003,112
PROR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 75
LENGTH: 206
                                                                                                                                                                                                                                                                    LOCATION: (1)..(206)
CTHER INFORMATION: X is selenocysteine
US-08-679-493A-75
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ERNST, Wolfgang
BALLANN, Claudia
PURTSCHER, Martin
TRKOLA, Alexandra
PREDL, Renate
SCHMATZ, Christine
KLIMA, Annelies
STEINDL, Franz
MUSTER, Thomas
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97.6%;
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Best Local Similarity 89.0%;
Matches 186; Conservative
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PRIOR FILING DATE: 1995
NUMBER OF SEQ ID NOS: 1
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Best Local Similarity
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                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-124-900-10
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SEQ ID NO 10
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TYPE: PRT
ORGANISM: Homo sapien
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                      -09-485-885-8
                                                                                                            APPLICANT:
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITS-- 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.4%; Score 597; DB 4; Length 383; 34.9%; Pred. No. 4.8e-52; Live 21; Mismatches 118; Indels 1
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
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                                                                                                                                                   Sequence 23, Application US/09485885 Patent No. 6342224
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Best Local Similarity 34.9
Matches 170; Conservative
400 TGPKETSGHHHHHH 413
                           269 ----VTSGHHHHH 278
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; ORGANISM: Homo sapien
US-09-485-885-23
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377 GHHHHHH 383
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US-09-485-885-23
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121 VVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNÅACAWLEAQEEEEVGFP 180
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Pred. No. 4.3e-52;
9; Mismatches 27;
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TILLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                              APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Cacherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT FILIG DATE: 2000-02-18
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 22
COURTAINS APPLICATION NOSER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
COURTAINS APPLICATION NOSER: GB 9717953.5
COURTAINS APPLICATION NOSER: GB 9717953.5
COURTAINS APPLICATION NOSER GB 9717953.5
COURTAINS APPLICATION NOSER GB 9717953.5
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FastSEQ for Windows Version 3.0
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Patent No. 6342224
Sequence 8, Application US/09485885
Patent No. 6342224
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ilarity 67.0%;
Conservative
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US-09-485-885-8
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Best Local Similarity
Matches 126; Conserv
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61 RLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 -----LERREVYDFA--------------------FRDLCIVYRDGNPYAVCDKCL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 -YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER 289
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                                                                                                                            360 ALGISYGRKKRRORRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 413
                                                                                                                                                                        ---ASOOTSGHHHHH 227
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34.9%; Pred. No. 2.4e-51;
Live 27; Mismatches 112; Indels 172;
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Dimbardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B6107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: US/09/485,885
PRIOR FILING DATE: 1998-08-17
PRIOR PLING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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          -- EEENDEIDEVN-
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US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 634224
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Best Local Similarity
Matches 167; Conserv
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                                                                                                                                                               1 MDPSSHSSNWANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDG
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                                                               Length 220;
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                                                                                                       Indels
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                                                             Score 593; DB 4;
Pred. No. 5.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.1%; Score 590; DB 4; 37.0%; Pred. No. 1.1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Buck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/FP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SSCTWARE: FastSEQ for Windows Version 3.0
LENGTH: 227
                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09485885
                                                          Query Match
26.2%;
Best Local Similarity 67.0%;
Matches 126; Conservative
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Best Local Similarity 37.0%
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapien
US-09-485-885-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Applicati
Patent No. 634224
GENERAL INFORMATION:
APPLICANT: Bruck, CI
APPLICANT: Cabezon 5
                                                                                                                                                                                                                                                                                                                                                                                  181 VTPQVPLR 188
                                                                                                                                                                                                                                                                                                                                                                                                                        155 AGQAEPDR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-485-885-16
US-09-485-885-1
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14;

9

12;

Gaps

Length 273;

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290 EVLEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCC 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KFYSKISEYR---------HYCYSLYGTTLE--QQYNKPLCDLLIRCINCQKPLCPEE 227
                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 -YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR PLING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
                                                                                                                                                                                                                                                                                                                                                                                  84; | Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG-----
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                                                                                                                                                                                                                                                                                                                                      Score 582; DB 4;
Pred. No. 9.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: ASSTSEQ for Windows Version 3.0
ENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 -AMFQDPQERPRKLPQLCTELQTTIHDI------
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                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                   25.7%;
ilarity 36.3%;
Conservative 24
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SEQ ID NO 74
LENGTH: 151
                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
US-09-485-885-4
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AFHHVARELHPE-YFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RLVVIHDHFLDGLTDVAKKFPHRHRKDGRYYVIDFTLKEIQSLEMTENFETMGGKWSKSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEAQEEEEVGFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDPSSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 --HLPARRAEPQRHTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 ALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHHHH 413
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----ASQQTSGHHHHH 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.9%; Score 587; DB 4;
36.7%; Pred. No. 2.3e-51;
Live 15; Mismatches 59
                                                                                                                                                         APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/FE98405285
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AMHGPKATLQDIVLH----
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
                                                                        Sequence 19, Application US/09485885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                       APPLICANT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 152; Conserv
                                                                                        Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GHNAD--
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APPLICANT:
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APPLICANT:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PARADO, CATI
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                               Indels
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PREDICATION NUMBER: US/08/450,257
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/235,403
FILING DATE: 21-MAY-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/937,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 29-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/454,650
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1991
APPLICATION NUMBER: Z7.794
RECISTRATION NUMBER: Z7.794
RECISTRATION NUMBER: Z7.794
RECISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           Score 498.5; DB 4;
Pred. No. 1.1e-42;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                          172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGG------
NAME/KEY: VARIANT
COCATION: (1)..(151)
COTHER INFORMATION: X is selenocysteine.
CS-08-679-493A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08450257
Patent No. S65212.
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 LEGL -- IHSQRRQDI-LDLWI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :|:: | | |||:
121 LPXLAELHTRARGGISTDLWM 141
                                                                                                                                                           Query Match 22.0%;
Best Local Similarity 73.0%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
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320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:

COUNTRY:

10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHIL RELEASE #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION STATE TO CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
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FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
APPLICATION NUMBER: PCT/US93/07833
TITING DATE: 19-AUG-1993
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APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-193
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
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TELERAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                 86 amino acids
                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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US-08-450-257-1
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                                                                                                                                                                                                                                                                                                                                     Length 86;
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APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PENINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     21.5%; Score 486; DB 1; 1
100.0%; Pred. No. 8.9e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                        human immunodeficiency virus
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1251 Avenue of the Americas
B170 CIP 2
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APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
APPLICATION NUMBER: US 08/158,015
APPLICATION NUMBER: US 08/158,015
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21-AUG-1992
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FILING DATE: 28-APR-1994
PAPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
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24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/450,098 FILING DATE: 25-MAY-1995 CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                   TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                TELECOMMUNICATION INFORMATION TELEPHONE: (212) 596-9000 TELEFRAX: (212) 596-9090
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       Query Match 21.59
Best Local Similarity 100.(
Matches 85; Conservative
                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TANUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York STATE: New "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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                                                                                                                                                                                                                                                           type 1
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                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                           US-08-450-246-1
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US-08-450-098-1
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320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPQG 379
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 86;
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APPLICANT: FRANKEL, Alan
APPLICANT: BABO, Carl
APPLICANT: PARSOUM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                  Score 486; DB 1; L
Pred. No. 8.9e-42;
O; Mismatches 0;
                                                                                                                                                                                                                                                                                                   human 1mmunodeficiency virus
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APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/058,766
FILING DATE: 19-AUG-1993
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
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STREET: 1251 Avenue of the Americas
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100.0%; Pri
tive 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                          TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                      REFERENCE/DOCKET NUMBER: B
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                         REGISTRATION NUMBER:
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Matches 85; Conserv
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US-08-450-098-1
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STATE:
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COUNTRY:
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Pred. No. 8.9e-42;
0; Mismatches 0; Indels
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APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENE ADDRESS:
ADDRESSEE: FISH & NEAVE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATE: US/08/450,236
FILING DATE: 28-MAY-1995
FILING DATE: US/07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US/07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US/07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US/07/08/376
FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: human immunodeficiency virus ; STRAIN: type 1 US-08-451-233-1
                                                                                     REGISTRATION UNDBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
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FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0;
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Patent No. 5804604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                    amino acid
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320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RILING DATE: 19911213
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.5%; Score 486; DB 1; L. 100.0%; Pred. No. 8.9e-42; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
TITLE OF INVENTION: RNA-Binding Proteins
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: human immunodeficiency virus
                                                            APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-5AN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/COCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11: 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
TELERAX: (212) 596-9000
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US O' / FILING PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07808452; Patent No. 6063612; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.(
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 86 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; STRAIN: type 1
US-08-450-236-1
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2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 61
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                                     380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                     62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                             Sequence 6, Application US/09124900
Patent No. 6268484
                                                                                                                                                                                                                                                                                                                   PREDL, Renate
SCHMATZ, Christine
KLIMA, Annelies
: STEINDL, Franz
: MUSTER, Thomas
                                                                                                                                                                                                                KATINGER, Hermann
BUCHACHER, Andrea
ERNST, Wolfgang
                                                                                                                                                                                                                                                                                     PURTSCHER, Martin
TRKOLA, Alexandra
PREDL, Renate
                                                                                                                                                                                                                                                                  SALLAUN, Claudia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapien US-09-451-905-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 19
LENGTH: 86
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LENGTH: 86
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                                                                                                                                                                                                                                                                                                        320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 86;
                                                                                                                                          the sequence of the TAT protein of HIV-1
                                                                                                                                                                                                                                  Length 86
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                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%; Score 486; DB 3; L
100.0%; Pred. No. 8.9e-42;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                Score 486; DB 3;
Pred. No. 8.9e-42;
                                                                                                                                                                                                                     21.5%; Sco...
100.0%; Pred. No. c...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: No. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09030613 Patent No. 6083706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 85; Conservative
                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 85; Conservative
                    86 amino acids
SEQUENCE CHARACTERISTICS
                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                        ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-07-808-452-1
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STATE: Washington
                    TOPOLOGY:
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                                                                                                                         ORIGINAL SOURCE
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                                                                                      HYPOTHETICAL:
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US-09-030-613-19
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320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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                                                                                                                                                                                                                                                                                                                                     0; Gaps
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APPLICANT: Andrew Baird
APPLICANT: Dale Baird
APPLICANT: Dale Baird
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
FILE REFERENCE: 200124,402C4
CURRENT APPLICATION NUMBER: US/09/451,905
CURRENT FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                  Length 86;
                                                                                                                                                                                                                                                               Ouery Match 21.5%; Score 486; DB 4; Length 86 Best Local Similarity 100.0%; Pred. No. 8.9e-42; Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                 ; ORGANISM: Human imunodeficiency virus type 1 US-09-124-900-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09451905 Patent No. 6306613
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PatentIn version 3.0
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320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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                                                                                                                               2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
21.5%; Score 486; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0; Indels
                             DB 4; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the sequence of the TAT protein of HIV-1
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9210770
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSED: SRI International
STREET: 313 Ravenswood Avenue
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10770
FILING DATE: 19921211
                         21.5%; Score 486; DB 4; I
100.0%; Pred. No. 8.9e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19921211
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY, AGENT INFORMATION:
NAME: Fablan, Gary R.
RECISTRATION NUMBER: P-2962
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 859-4550
TELEFAX: (415) 859-3880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                  Conservative
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21P: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: TEV
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                                           Best Local Similarity
Matches 85; Conserv
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HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                     RESULT 25
PCT-US92-10770-1
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                             Query Match
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                                                                             320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                           Gaps
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    Length 86;
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan

APPLICANT: PABO, Carl

APPLICANT: FAWELL, Stephen E.

APPLICANT: PERINKY, R. B.

TITLE OF INFORMATION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
Ouery Match 21.5%; Score 486; DB 4; I
Best Local Similarity 100.0%; Pred. No. 8.9e-42;
Matches 85; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/053/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 1-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1251 Avenue of the Americas STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B170 CIP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/235,403
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        Sequence 1, Application US/08235403
Patent No. 6316003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: human immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-235-403-1
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177 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 236
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF TITLE OF INVENTION: MAKING AND USES THEREOF FILE REFERENCE: 454310-3010 CURRENT APPLICATION NUMBER: US/08/815,809 CURRENT FILING DATE: 1997-03-12 NUMBER OF SEQ ID NOS: 23 SOFTWARE: PATENTIN Ver: 2.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 NYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH-GMDDPEREVLEW 294
                                                                                                                                                                                                                                                                                                          21.1%; Score 478.5; DB 3; Length 266; 77.3%; Pred. No. 2.7e-40; 11ve 4; Mismatches 6; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARTINE, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: WETHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERCE/CDOCKET NUBBER: 454310-2990
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/08816155B Patent No. 5990091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TARTAGLIA, JAMES APPLICANT: COX, WILLIAM I. APPLICANT: GETTIG, RUSSELL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 280 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Vaccinia virus US-08-815-809-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 745 FIL
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                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                  TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing S
TITLE OF INVENTION: and other Transactivating Strategies
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFIIKALGISYGRKKRRQRRRPPPG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                       Spring House Corporate Cntr, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RALease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.5%; Score 486; DB 5; 1
100.0%; Pred. No. 8.9e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                        Sequence 2, Application PC/TUS9506077 GENERAL INFORMATION:
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100.08; Pre-
                    62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-815-809-5; Sequence 5, Application US/08815809; Patent No. 6004777
                                                                                                                                                                                                                                                                                                              Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 11,215
REFERENCE/POCKET NUMBER: IR.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GETTIG, Russell R. APPLICANT: PINCUS, Steven E. APPLICANT: PAOLETTI, Enzo APPLICANT: JACOBS, Bertram L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TARTAGLIA, James
APPLICANT: GOEBEL, Scott J.
APPLICANT: COX, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.5
Best Local Similarity 100.
Matches 85; Conservative
                                                                                                                                                                  Immunobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO
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PCT-US95-06077-2
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                    CITY: Spring House
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                         19477
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210 NYTPGPGVRYPLTFGWCYKLVPM
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                                                                                                                                                            237 NYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH-GMDDPEREVLEW 294
                                                                                                                                                                                      APPLICANT: TARRAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GCTTIG, RUSELL R.
APPLICANT: GETTIG, RUSELL R.
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: RESENTING NEMENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STRATE: NEW YORK
                                                    17;
            Length 280;
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                                                    Indels
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        Score 478.5; DB 2;
Pred. No. 2.9e-40;
4; Mismatches 6;
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Pred. No. 2.9e-40;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERNCE/DOCKET NUMBER: 454310-2990
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/079,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10151
COMPUTER READABLE FORM:
COMPUTER: TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/09079587 Patent No. 6130066
    Query Match 21.1%;
Best Local Similarity 77.3%;
Matches 92; Conservative
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21.1%;
Best Local Similarity 77.3%;
Matches 92; Conservative
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US-09-079-587-43
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177 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 236

Indels

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237 NYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH-GMDDPEREVLEW 294

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                                                                 APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P:
STREET: 1737 King Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 EPVDPRLEPWKHPGSQPKTACINCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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Pred. No. 3.7e-40;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: FILPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,210
FILNG DATE: 14-AuG-1995
PLIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/215,248
FILING DATE: 21-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/215,248
FILING DATE: 11-MAR-1994
ATPONENTY-APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/01457
FILING DATE: 13-DEC-1994
ATRONEY-APPLICATION DATA:
ANAME: DAGING SAMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: Lai
INDIVIDUAL ISOLATE: sequence of the TAT protein
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Sequence 1, Application US/08505210
Patent No. 5981258
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, S
STREET: 1737 King Street,
CITY: Alexandria
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96.5%;
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    Virginia
: United States
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STRANDEDNESS: si
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Best Local Similarity
Matches 82; Conserv
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ORIGINAL SOURCE:
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Search completed: August 26, 2002, 08:10:41 Job time: 130 sec

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FUB;
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(without alignments)
395.919 Million cell updates/sec
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human immun
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2264
1 MDPSSHSSNWANTQMKSDKI......QSRGDPTGPKETSGHHHHHH 413
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Copyright (c) 1993 - 2000 Compugen Ltd.
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EMBL: U12055; AAA76691.1; -.
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P03406; 1EFN.
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Q70627;
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HSSP; P0340
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"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
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MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky
IIV; KO2013; NEFSBRU.

IIV; M19921; NEFSNL43.

IIV: M19921; PRO01558.

IIV: PF00469; Fprotein; 1.

IIDS; Myristate; GTP-binding; Phosphorylation; 3D-structure.
                                                                                                                                                      Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11700;
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T -> A (IN CLONE PNL4-3).

A -> V (IN CLONE PNL4-3).

T -> N (IN CLONE PNL4-3).

77453FC80B6004F2 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                 PHOSPHORYLATION (BY PKC)
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Pred. No. 1.4e-86;
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Nature 313:450-458(1985).
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100.0%; Pred
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Nature 330:266-269(1987).
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AC PO3405;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-9733745; Pubmed-9194185;
MEDLINE-9733745; Pubmed-9194185;
Gressiek S., Bax A., Hu J.S., Kaufman J., Palmer I., Stahl S.J.,
Tjandra N., Wingfield P.T.;
"Refined solution structure and backbone dynamics of HIV-1 Nef.";
Protein Sci. 6:1248-1263(1997).
-!- FUNCTION: WEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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206 AA; 23352 MW; EDE64281A17C6735 CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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Pred. No. 3e-85;
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-; NOT_ANNOTATED_CDS
                                                                          HIV; K02083; NEF$PV22.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
LIPID 2 2 MYIS
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                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an oncogene product.";
Nature 330:266-269(1987)
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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MEDLINE-88039140; PubMed-3118220;
GUY B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-86177573; PubMed-3008154;

Arya S.K., Gallo R.C.;

"Three novel genes of human T-lymphotropic virus type III: 1
reactivity of their products with sera from acquired immune
deficiency syndrome patients.";

Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
                                                                                                Length 206;
                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus typė 1 (clone 12) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                              MYRISTATE.
; ED81F68F6861278E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                            Query Match
49.1%; Score 1111; DB 1;
Best Local Similarity 97.1%; Pred. No. 5.4e-85;
Matches 200; Conservative 5; Mismatches 1;
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Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding; 3D-structure.
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HSSP; P03406; IEFN.
HIV; M11840; NIFFSPCV12.
InterPro; IPR001558; F-protein.
                                                          206 AA; 23414 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11679;
                                                                                                                                                                                                                                                                                                                                                                                   NEF_HV112
P04324;
                                              LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            RESULT 4
NEF_HV112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling an oncogene product."
Nature 330:266-269(1987)
-i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
                                                                                                                                                                                                                                                                  112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                            QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
                                                                                                                                                                                                                                                                                                                                                                                                           61 QEEEKVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY 120
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                              MEDLINE-85111123; PubMed-2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1985).
                                                                                                                                                           Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HIV-1).
                                                                                                                                                                                                                   Indela
                                                    MYRISTATE.
; 218F5B2980F79A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (BH8 isolate) (
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11684;
                                                                                                                                                              DB 1;
                                                                                                                                                         Score 1108; DB 1;
Pred. No. 9.5e-85;
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 09, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEWRFDSRLAFHHVARELHPEYFKNC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEWRFDSRLAFHHVARELHPEYFKNC
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
                                                                           206 AA; 23366 MW;
                                                                                                                                                              48.98;
97.18;
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.1
Matches 200; Conservative
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SEQUENCE FROM N.A.
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEF_HV1B8
P05855;
                                                                           SEQUENCE
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Matches 185;
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P19545;
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                                                                                               ä
                                                                                                                                                                                                                       291
                                                                                                                                                                                    231
                                                                                                                      112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-89085613; PubMed-2789516; Anand R., Thayer R., Luciw P., Dandekar S., Gardner M., Luciw P., Dandekar S. and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive
                                                                                                                                  1 MGGKWSKSSVVGWPAVRERMRRAEPPADGVGAVSRDLEKHGAITSSNTAATNADCAMLEA 60
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITOLOGY 168:79-89(1989).
-I-FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-I-MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
                                                                                                                                                                                                                    FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                      172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                               Ä
                                                                      Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11693;
                                                                     Score 1088.5; DB 1; Length
Pred. No. 3.9e-83;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 2 MYRISTATE (BY SIMILARITY)
218 AA; 25032 MW; FC4DAEA1045C460E CRC64;
                                  8EC12F6650DDD111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-07T-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 KDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                          218 AA
                       MYRISTATE
                                                                                                                                                                                                                                                                                 180 LEWRFDSRLAFHHMARELHPEYFKNC 205
                                                                                                                                                                                                                                                                     292 LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 2.
                                 205 AA; 23305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS; Myristate; GTP-binding.
AIDS; Myristate; GTP-binding.
LIPID
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                                                                     Query Match
Best Local Similarity 96.6%;
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P03406; 1EFN.
HIV; M21098; NEF$BRVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P12479;
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                                  SEQUENCE
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NEF_HV1BN
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Length 218;

Score 1019; DB 1; Pred. No. 2.4e-77;

45.0%; 84.1%;

Query Match Best Local Similarity

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                                                                                                                                                                   NTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRR 217
                                                                                                                                                                                                QDILDLWIYHTQGYFPDWQNYTPGFGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLH 277
                                                                                                                                                                                                                                                                                                              ----RAEPAADGVGAASRDLEKHGAITSS 157
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     Gaps
                                                                                 MEDILNE-90317906; PubMed-2370688; Park Higglins D., Cheng-Maper C., Bauer D., Levy J.A., Dina D.; York-Higglins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.; York-Higglins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.; Feplication, and cytopathicity are linked to the envelope region of the viral genome., J. J. Virol. 64:4016-4020(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11690;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYRISTATE (BY SIMILARITY). FFB419A1C5DFC9F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 KDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                          278 PVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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  12;
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                                                       MGGKWSKSSVVGWPTVRERMR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M38427; AAA45068.1; -. HSSP; P03406; 1EFN.
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; M38427; NEF$SF33.
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                                                                                                                                                                                                                                                                                                                                                                                                                            POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
MEDLINE-88039140; PubMed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 167
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-85090453; PubMed-2578227;
Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
Stemplen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
Stemplen M.M., D., Lucim P.A.;
Levy J.A., Dina D., Lucim P.A.;
"Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOGY PDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                        Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%; Score 997; DB 1; Length 210;
85.2%; Pred. No. 1.5e-75;
ive 16; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE.
ED255233F8A17DAB CRC64;
                                                            21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
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    210 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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HIV; KO2007), WEFSSFS.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24042 MW;
                                            21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an oncogene product.";
Nature 330:266-269(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K02007; AAB59883.1; -. PIR; A04009; ASLJO2.
                                                                                                                                                                                                                                                                                                                                                                                        Science 227:484-492(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.29
Matches 179; Conservative
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    STANDARD;
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SEQUENCE
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NEF_HV1RH
ID NEF_HV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 MGGKWSKSSVVGWPTVRERMRRA----EPAADGVGAASRDLEKHGAITSSNTAATNAAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 226
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110 FPDWQNYTPGPGVRFPLTFGWCFKLVPVEPEKVEEANEGENNSLLHPMSLHGMEDPEKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-90148544; Pubmed-2559749;
Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S. Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S. Halghly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: NEF HÁS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-!- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.
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                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
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82.9%; Pred. No. 1.4e-75;
ive 22; Mismatches. 9;
                                                                                                                                                                                                                211 AA.
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                                                                                     180 LVWKFDSHLAFRHWARELHPEYYKDC 205
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
                                                              292 LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AA; 24067 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M26727; AAA83398.1; -.
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Matches 175; Conservative
                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                              NEF_HV10Y
P20886;
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Gaps

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RESULT 9

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NEF_HV1JR
P20867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q -- EEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQ 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    itted (XXX-1987) to the HIV data bank. FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-93021387; PubMed-1404605;
Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                    (RF/HAT isolate) (HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=36377;
                                                                                                               SEQUENCE FROM N.A.
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S
Woolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
Wong-Staal F.;
Submitted (XXX-1987) to the HIV data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
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8F836FE8980F084C CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                    01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                  Human immunodeficiency virus type 1 (RF/HAT isolate
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 994; DB 1;
84.6%; Pred. No. 2.7e-75;
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                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 1, AIDS; Myristate; GTP-binding.
            Created)
                                                                                                                                                                                                                                                                                                                                                                                         208 AA; 23532 MW;
                                                                                                                                                                                                                                                                                                        EMBL; M17451; AAA45058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 84.6
Matches 176; Conservative
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         (Rel. 09, C
                                                                                                                                                                                                                                                                                                                               HIV; M17451; NEFSRF
                                                                                         NCBI_TaxID=11701;
         1-NOV-1988
1-NOV-1988
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P35959;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 MGGKWSKSSVVGWPTVR-----ERMRRAEPAADGVGAASRDLEKHGAITSSNTAA 161
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"Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";
J. Virol. 66:6587-6600(1992).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koyanagi S., Chen I.S.Y.;
Submitted (DEC-1988) to the HIV data bank.
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN'REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 991.5; DB 1; Length 214; Pred. No. 4.5e-75; Mismatches 11; Indels 11.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYRISTATE (BY SIMILARITY).
E188D43D7B084D04 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 HGMDDPEREGLEWRFDSRLAFHHVARELHPEYYKN 214
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84.2%; Pre
tive 12;
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InterPro; 1PR001558; F-protein.
Pfan; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA; 24532 MW;
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Matches 181; Conservative
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Local Simines 176;
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                                                                                                                                                                                                                           RESULT 14
NEF_HV1EL
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           Matches
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                                                                                                                                                                                                                         162 TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL 221
                                                                                                                                                                                                                                                         DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 281
                                                                                                                                                                  112 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 161
                                                                                                                                               Gaps
                                                                                                                                                                              Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;

"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";

J. Virol. 64:4390-4398(1990).

-I- FUNCTION: NEF HAS GIPASE, GIP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  numman immunodeficiency virus type l (SF162 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11691;
                                                                                                                        Length 216;
                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYRISTATE (BY SIMILARITY); A0B1007D14E46E32 CRC64;
                                                                           MYRISTATE (BY SIMILARITY)
D163FFA8C71529DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                     43.3%; Score 981; DB 1;
81.9%; Pred. No. 3.4e-74;
iive 15; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                              NEF_HVISI STANDARD, PRT; 208 AA. P19546. 01-FEB-1991 (Rel. 17, Created) 10-FEB-1991 (Rel. 17, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                               HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-90347835; PubMed-2384920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                              HIV; M38429; NEF$JRCSF.
InterPro; IPR001558; F-protein.
                                                                                      216 AA; 24567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23684 MW;
                                                   Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
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          EMBL; M38429; AAB03750.1;
HSSP; P03406; 1EFN.
                                                                                                                                Best Local Similarity 81.9
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV; M38428; NEF$SF162.
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                                                                                      SEQUENCE
                                                                                                                        Query Match
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Length 208;

43.0%; Score 974; DB 1;

Query Match

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MEDLINE-88039140; Pubmed-3118220;
Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                         MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 168
                                                                                                                                                                                                                                                                                                                      QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE-86245056; PubMed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
Cell 46:63-74(1986).
                                               Gaps
                                                                                                                                                        1 MGGKWSK-RMSGWSAVRERMKRAEPAEPAADGVGAVSRDLEKHGAITSSNTAANNADCAW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an oncogene product.";
Nature 330:266-269(1987).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                             LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11689;
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                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
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79.1%; Pred. No. 8.5e-70;
iive 24; Mismatches 18;
                      1.2e-73;
thes 13;
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                      Pred. No. 1.2e; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 KEVLVWRFDSRLAFHHMARELHPEYYKDC 208
                                                                                                                                                                                                                                                                                                                                                                                                                              289 REVLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
84.28; F1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23612 MW;
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                      Similarity 84.2%
6; Conservative
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Best Local Similarity 79.1
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Pfam; PF00469; F-
AIDS; Myristate;
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P04604;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Lecocq J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                   230
  MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 330:266-269(1987).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                           QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Srinivasan A., Anand R., York D., Ranganathan P., Feorino Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC095A1B263047CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Negative factor (F-protein) (27 kDa protein) (3'ORF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                   291 VLEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                         MEDLINE-87248097; PubMed-3036660;
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HSSP, P03406; IEFN.
HIV; K03438; NEFSZ6.
InterPro; IPR001558; F-protein.
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Sanchez-Pescador R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 52:71-82(1987).
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ID NEF_HV126
AC P04602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 81:275-284(1989).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- MISCELLANEOUS: NOK, ISOLATED FROM A ZAIRTIN PATIENT AFFECTED WITH
AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 QEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90034200; PubMed-2806917; Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.; More A., Chermann J.C.; More B., Chermann J.C.; More B., Chermann J.C.; More B., Chermann of HIVI-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                 YHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMD 285
                                                                                                                                                                                                                                                                      12 MGGKWSKSSVVGWPTVRERM-----RRAEPAADGVGAASRDLEKHGAITSSNTAATNAAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                     1 MGGRWSKSSIVGWPAIRERIRRTDPRRTDPAADGVGAASRDLEKHGAITSSNTRDTNADC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA
                                                                                                                                                                                                                                                                                                                                                           HSSP, P03406; IEFN,
HIV; M27323; NEFSNDK.
InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA; 23748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M27323; AAA44874.1; -. PIR; JQ0068; QQLJND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00469; F-protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.38
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEF_HV1ND
P18801;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 MGGKWSKSSVVGWPTVRERMRRAEP---AADGVGAASRDLEKHGAITSSNTAATNAACAW 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGGKWSK-RVIGWPIVRERMRRAEPAELAADGVGAASRDLEKHGALISSNIAAINADCAW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-89228766; PubMed-2713163;
Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11692;
                                                                                                                                                                                                                                                                                                                       OGYFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11696;
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2C5B5A6E3EF13B26 CRC64;
                                                                                                                                                  Negative factor (F-protein) (27 kDa protein) (3'ORF).
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(Rel. 40, Last annotation update)
                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
      182 AA.
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InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
LIPID 2 2 MYS
SEQUENCE 182 AA; 20632 MW; 2
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01-NOV-1988 (Rel. 09, Last seq
16-OCT-2001 (Rel. 40, Last anno
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87.4%;
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      STANDARD;
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Matches 153; Conserv
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P05859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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YFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPERE 290
                               112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of a Ugandan HIV-1 provirus reveals genetic diversity from other HIV-1 isolates."; AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
-:- FUNCTION: NEF HAS GIPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
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869AB03E6E7893C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11703;
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                                                                                                                                                                                                                                                                                                                              205 AA.
                                                                                                                   291 VLEWRFDSRLAFHHVARELHPEYFKNC 317
                                                                                                                                                  292 LEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91090981; PubMed=2265025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001558; F-protein.
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LMWKFDSTLALKHRAYELHPEFYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 AA; 23253 MW;
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P24741;
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RESULT 17

NEF\_HV1U4

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16-OCT-2001
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P17664;
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88039140; PubMed-3118220; Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M., Montagnier L., Lecocq J.-P.; "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 MGGKWSKSSVVGWPTVRERMRR---AEPAADGVGAASRDLEKHGAITSSNTAATNAACAW 168
                                                                                                                                                                                                                                                                                                                                                                                                                                         LEAGEE-EEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alizon M., Wain-Hobson S., Montagnier L., Sonigo P., "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     collected
                                             AIDS Res. Hum. Retroviruses 5:121-129(1989).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                   ..
80
CCOIMICK J., Ou C.Y., Myers G., Smith T., Chen E.; Molecular characterization of HIV-1 isolated from a serum
                                                                                                                                                                                                                                                                                                                                         Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11697;
                         nucleotide sequence comparison to recent isolates
                                                                                                                                                                                                                                                                                                                                                                  25; Indels
                                                                                                                                                                                                                                                                                        MYRISTATE (BY SIMILARITY)
EA55B18AF412A9D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                                                                                                                                        37.0%; Score 837; DB 1; 73.2%; Pred. No. 2.7e-62; 1ve 23; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EREVLEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 EREVLMWKFDSSLARKHLAREMHPEFYKD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86245056; PubMed-2424612;
                                                                                                                                                                                                              PIR; B44963; B44963.
HSSP; 903406; IERN.
HIV; M15896; NIEF$2321.
InterPro; IPR001558; F-protein.
                                                                                                                                                                                                                                                                                                205 AA; 23306 MW;
                                                                                                                                                                                                                                                             Pfam; PF00469; F-protein; 1. AIDS; Myristate; GTP-binding.
                                                                                                                                                                                                  EMBL; M15896; AAB53951.1; -.
                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 73.23
Matches 153; Conservative
                                        generation of hybrid HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEF_HV1MA
P04603;
                                                                                                                                                                                                                                                                                                    SEQUENCE
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NEF_HV1MA
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 AWLEAQEEEEVGFPVTPQVPLRPMTYRAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E--PPEEEEEVGFPVRPQVPLRPMTYKGAFDLSHFLKEKGGLDGLVWSPKRQEILDLWVY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Huet T., Cheynler R., Meyerhans A., Roelants G., Waln-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 346:356-359(1990)
-i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 330:266-269(1987).
-!- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 2 MYRISTATE.
209 AA; 23644 MW; D0B30A2442CBCC44 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 834.5; DB 1 Pred. No. 4.4e-62;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Scor.
70.1%; Pred. No. 4...
''A 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
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                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04415; CAA28017.1; -.
BMBL; AO7116; CAA00624.1; -.
HSSP; P03406; IEFN.
HIV; K03456; NEFSMAL.
InterPro; IPR001558; F-protein.
Pfam; PP00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
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Query Match
Best Local Simi
Matches 157;
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NEF_HV1H2
                                                                   112
                                                                                                                                    61
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  231
                                                                                                                                                                                                                                                                      291
                                                                                                                                                                              112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                          Gaps
                                                                                                                                                                                          Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
Farrell, K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
"Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
-: FUNCTION: NEF HAS GYPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-: FUNCTION: NEF MAS GYDAM-REGULATE THE CD4(TQ4) ANTIGEN.
-: MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
                                                                                                                                                                                                                            QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                        FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                          ö
                                                                                                                                    Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11702;
                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 2 MYRISTATE (BY SIMILARITY).
239 AA; 26799 MW; 704A17E54763A99B CRC64;
                                                                                       MYRISTATE (BY SIMILARITY)
21E0A3EC99F1811F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                 ); Score 832; DB 1;
); Pred. No. 6.9e-62;
27; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                292 LEWRFDSRLAFHHVARELHPEYFKN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88219542; PubMed-3369091;
        EMBL; X52154; CAA36408.1; -, PIR; S09991; ASLJIK. HSSP; P03406; IEPN. HIV, X52154; NEFSCPZ. InterPro; IPR001558; F-protein. Pfam; PF00469; F-protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1984 IN SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; Myristate; GTP-binding.
                                                                                                205 AA; 23850 MW;
                                                                                                                                  36.78;
70.28;
                                                                            AIDS; Myristate; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M17450; AAA45064.1; -.
                                                                                                                                 Ouery Match
Best Local Similarity 70.2
Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV; M17450; NEF$SC
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                                                                                                                                                                                                                                                                                                                                                                                                NEF_HV1SC
P05857;
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-!- MISCELLANEOUS: IN THIS ISOLATE A WUTATION IN POSITION 124 ADDS A STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES (210 AA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88039140; PubMed-3118220; Guy B., Kieny M.-P., Riviere Y., le Peuch C., Dott K., Girard M., Montagnier L., Lecocq J.-P.; "HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                             232 FPDWQNYT--PGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPER 289
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87299196; PubMed-3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F. "Complete nucleotide sequences of functional clones of the AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R. -S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11706;
DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou
Gallo R.C., Wong-Staal F.;
                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEF_HV1H2 STANDARD; PRT; 123 AA. P04601; 009780; 13-406-1987 (Rel. 05, Created) 115-JUL-1999 (Rel. 38, Last sequence update) 116-JUL-1999 (Rel. 40, Last annotation update) Negative factor (F-protein) (27 kDa protein) (3'ORF).
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POST-TRANSLATIONAL MODIFICATIONS, AND FUNCTION.
Score 819; DB 1
Pred. No. 1e-60;
; Mismatches
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                                                           16;
36.2%;
75.5%;
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Nature 330:266-269(1987).
                                                           Conservative
                             Similarity
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REVISIONS.
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Escherichia coli.
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                                                                                                          LIPID
SEQUENCE
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MEDLINE-88039140; PubMed-3118220;
Guy B., Kiany M.-P., Riviere Y., le Peuch C., Dott K., Girard M.,
Montagnier L., Leccog J.-P.;
"HIV F/3' orf encodes a phosphorylated GTP-binding protein resembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
-i- MISCELLANEOUS: IN THIS ISOLATE A WITATION IN POSITION 124 ADDS A STOP CODON AND THE PROTEIN IS MUCH SHORTER THAN IN OTHER ISOLATES
                                                                                                                                                                                                                                                                                                                                                                                                    112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       MEDLINE-85111123; PubMed-2578615;
Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong-Staal F.; "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                       Length 123;
                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                PHOSPHORYLATION (BY PKC).
B5007753CCD244CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.-UL-1986 (Rel. 01, Created)
13.-MGG-1987 (Rel. 05, Last sequence update)
16.-CCT-2001 (Rel. 40, Last annotation update)
Negative factor (F-protein) (27 kDa protein) (3'ORF).
                                                                                                                                                                                                                       28.5%; Score 645; DB 1; 98.4%; Pred. No. 1.1e-46;
HIV; K03455; NEFSHXB2.

InterPro; IPR001558; F-protein.

Pfam; PF00469; F-protein; 1.

AIDS; Myristate; GTP-binding; Phosphorylation.

MYRISPANDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AA
                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                MOD_RES 15 15 P
SEQUENCE 123 AA; 13692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M15654; AAA44206.1; -.
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                                                                                                                                                                                                                                                                       Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 313:277-284(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an oncogene product.
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HSSP; Q70627; 2NEF.
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 FPD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||
|121 FPD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEF_HV1B1
P03404;
                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEF_HV1B1
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                  NO NA TEL
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycerophosphoryl diester phosphodiesterase precursor (EC 3.1.4.46)
(Glycerophosphodiester phosphodiesterase) (Surface-exposed lipoprotein
D) (Protein D) (Immunoglobulin D-binding protein) (IGD-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-MINNA / SEROTYPE B;
MEDLINE-94011360; Pubmed-8104899;
MEDLINE-94011360; Forsgren A.;
Janson H., Ruan M., Forsgren A.;
"Limited diversity of the protein D gene (hpd) among encapsulated and nonencapsulated Haemophilus influenzae strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMHYHTYGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Weidmen J.E., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                   112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
                                                                                                                                                                                                                                                                                                                        Gaps
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Janson H., Heden L.-O., Grubb A., Ruan M., Forsgren A.;
"Protein D. an immunoglobulin D-binding protein of Haemophilus
influenzae: cloning, nucleotide sequence, and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                      Length 123;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                MYRISTATE. 0811735345F0EB8B CRC64;
                                                                                                                                                                                                                                                                                                                     ٠<u>.</u>
                                                                                                                                                                                                                                                      Score 638; DB 1;
Pred. No. 4.2e-46;
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                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95350630; PubMed-7542800;
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HIV; M15654; NEFSBH102.
InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS: Myristate; GTP-binding.....
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STRAIN-RD / KW20 / ATCC 51907;
                                                                                                                                                             123 AA; 13606 MW;
                                                                                                                                                                                                                                                      28.2%;
ilarity 97.6%;
Conservative
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GLPQ OR HPD OR HI0689.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 120; Conserv
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364
364 AA;
                                                                                                                           Query Match
Best Local Similarity
Matches 141; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 ESKPDNI 299
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  253
310
327
                                                   338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAT_HV1B1
P04606;
                                                                           VARIANT
SEQUENCE
             VARIANT
VARIANT
  VARIANT
                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                              247
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                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  PTM: CONTAINS BOTH ESTER- AND AMIDE-LINKED FATTY ACIDS.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAINS NTHI 772 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACYL DIGLYCERIDE.

A -> T (IN STRAIN NCTC 8468).

N -> V (IN STRAIN NCTC 8468).

N -> V (IN STRAIN NCTC 8468).

N -> K (IN STRAIN NCTC 8468).

N -> H (IN STRAIN 6-7626).

H -> Q (IN STRAIN 8-7626).

S -> A (IN STRAINS EAGAN; 3639; 3640;

NCTC 8468; 6-7626; MK695; MINNA).

Y -> H (IN STRAINS EAGAN; 3639; 3640;

NCTC 8468; 6-7626; MK695; MINNA).

Y -> H (IN STRAIN NCTC 8468).

K -> Q (IN STRAIN 6-7626).

K -> Q (IN STRAIN 6-7626).

K -> A (IN STRAIN 6-7626).

T -> A (IN STRAIN 6-7626).

NCTC 8468; 6-7626; K695; MINNA).
                                                                                                                                              MEDITRE-91192801; PubMed-1548059;
Janson H., Heden L.-O., Forsgren A.;
Forschin D., the immunoglobulin D-binding protein of Haemophilus
influenzae, is a lipoportein.;
Infect. Immun. 60:1336-1142(1992).
Infect. Immun. 60:1356-1142(1992).
Infect. FUNCTION: GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE HYDROLYZES
DEACYLAYED PHOSPHOLIPIOS TO G3P AND THE CORRESPONDING ALCOHOLS.
HAS A SPECIFIC AFFINITY FOR HUMAN IMMUNOGLOBULIN D WYELOMA
                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: A glycerophosphodiester + H(2)O = an alcohol sn-glycerol 3-phosphate.
SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR004129; GDPD.
Pfam: PF03009; GDPD: 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Glycerol metabolism; Hydrolase; Signal; Lipoprotein; Outer membrane;
                                                             Song X.-M., Forsgren A., Janson H.;
"The gene encoding protein D (hpd) is highly conserved
"Aemophilus influenzae type b and nontypeable strains."
Infect. Immun. 63:696-699(1995).
                                     6-7626, AND HK695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE.
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO E.COLI AND B.SUBTILIS GLPQ.
                       SEQUENCE FROM N.A.
STRAIN-EAGAN, 3639, 3640, NCTC 8468,
MEDLINE-95122210; Pubmed-7822043;
Infect. Immun. 61:4546-4552(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA84715.1;
CAA84716.1;
CAA84717.1;
CAA84718.1;
CAA84719.1;
CAA84719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32751; AAC22348.1; -.
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AAA24999.1; -.
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364
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119
225
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144
168
191
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                                                                                                                          CHARACTERIZATION.
                                                                                                                                         STRAIN-NTHI 772;
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116
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62
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                                                                                                                                                                                                                                                                                                                                             / KW20
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VARIANT
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                                                                                                                                                                                                                                                                                                            ---SKSSVVG-WPTVRERMRRAEPAADGVGAASRDLEK 150
                                                                                                                                                                                                                                                                                                                                                                                140 FPLWKSHFRIHTFEDEIEFIQGLEKSTGKKVGIYPEIKAPWFHHQNGKDIATETLKVLKK 199
                                                                                                                                                                                                                                                                                                                                                                                                                            HGAITSSNTAATNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 LIHSQRRQDILDLWIYHTQGYFPDWQ------NYTPGPGVRYPLTFGWCYKLVPVE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73; Gaps
                                                                                                                                                                                                                                                 20 SSHSSNWANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQHSDYLEQDLAMTKDGRLV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P -> S (IN STRAIN 6-7626).
Q -> K (IN STRAIN 6-7626).
E -> A (IN STRAINS EAGAN; 3639; NCTC
8468; 6-7626; HK695; MINNA).
A -> V (IN STRAINS EAGAN; 3640; HK695;
MINNA).
                                                                                                                                                                                                                               4 SSHSSNMANTQMKSDKIIIAHRGASGYLPEHTLESKALAFAQQADYLEQDLAMTKDGRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGYDKKTD-----MVYLQTFDFNELKRIKTELLPQMGMDLK-LVQLIAYTDWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1), and Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11678, 11707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ISOLATE BH10;
MEDLINE=83111123; Pubmed=2578615;
Rathor L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.
JOSEPHS S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo
                                                                                                                                                                Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
                                                                                                                                                                                                Indels
                                                                                                -> E (IN STRAIN 6-7626)
A6079B3ABF70E820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                              ; Score 553.5; DB 1;
; Pred. No. 1.7e-38;
21; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA.
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Σ
                                                                                                                                                              24.4%;
ilarity 45.9%;
Conservative 21
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41902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 313:277-284(1985)
     253
310
327
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86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                  TAT_HV112
P04326;
                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Nature 313:460-458(1985).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                       320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85111157; PubMed-2982104;
Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                  -! - SUBCELLUIAR LOCATION: NUCLEAR; NUCLEGLAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses: Retroid viruses: Retroviridae; Lentivirus.
NCBL_TaxID=11700;
                                                                                                                                                                                                                                                                                                                                                                    21.5%; Score 486; DB 1; Length 86; 100.0%; Pred. No. 1e-33; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           86 AA; 9784 MW; 4DD609415FAF9015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                          PROMOTER. SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
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-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                     PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                          IPR001831; HIV_Tat.
                                                                                                                                                                                                     EMBL; M14100; AAA44676.1; -.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 85; Conservative
                                                                                                                                                                                                                   EMBL; M15654; AAA44199.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                 HIV; M15654; TAT$BH102.
HIV; M14100; TAT$HXB3.
                                                                                                                                                                                                                                                                       Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAT_HV1PV
ID TAT_HV1PV
AC P04607;
                                                                                                                                                                                                                                                             interPro;
                                                                                                                                                                                                                                                                                                                AIDS.
SEQUENCE
                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capon
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                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                             Score 481; DB 1; Length 86;
Pred. No. 2.7e-33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBL_TaxID=11679;
                                                                                                                                                                                                                        9794 MW; 4DD5C6415FAF9015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4DD609414FBE9115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 AA.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                             EMBL; X01762; -; NOT_ANNOTATED_CDS HIV; K02083; TAT$PV22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 SQTHQVSLSKQPTSQPRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 04, Created)
(Rel. 05, Last seq
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                                                                                                                                                        PRINTS; PR00055; HIVTATDOMAIN
                                                                                                           InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M11840; AAA44999.1; -..
PIR; A04017; TNLJ12.
HIV; M11840; TAT$PCV12.
                                                                                                                                                                                                                                                                                           21.2%;
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                                          EMBL; K02083; AAB59870.1;
                                                                                                                                                                                                                                                                                                                                        84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                          86 AA;
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21.1%; Score 478; DB 1; Length 86;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
Submitted (JUN-1988) to the EMBL/Genbank/DDBJ databases
--- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
--- FUNCTION: TRANSCRIPTION INTITATION AND/OR ELONGATION FROM THE LTR
                                           320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
                                                            2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRAPGG 61
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator; RNA-binding; Nuclear protein;
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T -> M (IN CLONE PNL4-3).

PPGG -> AHON (IN CLONE PNL4-3).

P -> A (IN CLONE PNL4-3).

P -> S (IN CLONE PNL4-3).

9B1B4A915FAF8A14 CRC64;
                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus. (VCBL_TaxID-11686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 470; DB 1; Length 86
Pred. No. 2.2e-32;
); Mismatches 3; Indels
                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Alizon M.;
                                                                                                                                                                                                                                                                                TAT protein (Transactivating regulatory protein).
Pred. No. 4.7e-33;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85099333; PubMed-2981635; Wain-Hobson S., Sonigo P., Danos O., Cole S., i Nucleotides sequence of the AIDS virus, LAV."; Cell 40:9-17(1985).
                                                                                                                                                                                                                                   (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                            86 AA
                                                                                                                                                                                                         PRT;
                                                                                                   380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (CLONE PNL4-3).
                                                                                                                     62 SQTHQVSLSKQPTSQSRGDPTGPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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96.5%;
98:86
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Best Local Similarity 98:8
Matches 84; Conservative
                                                                                                                                                                                                            STANDARD;
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39
61
67
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HIV; M19921; TAT$NL43.
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                                                                                                                                                                                                                                     13-AUG-1987 (
13-AUG-1987 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                         TAT_HV1BR
P04610;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 45:637-648(1986).
-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING TESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                   "identification and characterization of conserved and variable regions in the envelope gene of {\rm HTLV-III/LAV}, the retrovirus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86218077; Pubmed-2423250;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.4%; Score 461; DB 1; Length 102; 91.9%; Pred. No. 1.5e-31;
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                                                                                                                                                                                                                            !AT protein (Transactivating regulatory protein).
                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                102 AA
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                                                                                                                                PRT;
380 SQTHQVSLSKQPTSQSRGDPTGPKE 404
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                     62 SQTHQVSLSKQPTSQPRGDPTGPKE
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InterPro; IPR001831; HIV_Tat.
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                                                                                                                                  STANDARD;
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Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Wong-Staal F
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                                                                                                                            TAT_HV1RH
P05908;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                            FAT_HV1RH
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Search completed: August 26, 2002, 08:15:43 Job time: 347 sec

EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 379

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2 EPVDPRLEPWKHPGSQPKTACTTCYCKKCCFHCQVCFTTKALGISYGRKKRQRRRPPGG 61

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(A Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,

(A Visco Comandini U., Yun Z., Paganelli R., Orlandi P., Salotti A.,

Johansson B., Vahlne A., Sonnerborg A.;

Johansson B., Vahlne A., Sonnerborg A.;

"HIV-1 nef mutations and clinical long-term non progression: a

"Though a mutation of the EMBL/GenBank/DDBJ databases."

"Le SIMILARITY: NEF HAS GTPAER, GTP-BINDING AND AUTOPHOSPHORYLATING

"L. SIMILARITY: NEF HAS GTPAER, GTP-BINDING AND AUTOPHOSPHORYLATING

"ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

"REMBL, AF011480; AAD01458.1; -..

RHSSP, P03406; LEFN.

RHSSP, P034066; LEFN.

RHSSP, P034066; LEFN.

RHSSP, P034066; LEFN.

RHSSP, P034066; LEFN.
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 3.6e-83;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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molecular clone.";
J. Virol. 59:284-291(1986).
Bebri U26942; AAB60579.1; -.
SEQUENCE 206 AA; 23367 MW;
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Best Local Similarity
Matches 203; Conserv
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AIDS: GTP-binding; Myristate.
SEQUENCE 206 AA; 23341 MW; FCD22B1CEB655BB9 CRC64;
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Last annotation update)
(27 KDA PROTEIN).
                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                49.6%; Score 1124; DB 15; 99.0%; Pred. No. 9.2e-83; iive 1; Mismatches 1;
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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MEDLINE=96036482; PubMed=7483282;
Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
Michael N.L., Carr J.K., Burke D.S., McOutchan F.E.;
Mecovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
Virology 213:80-86(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                                                                                                                                                                                                                Submitted (MAY.1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP: P03406; 1EFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGGKWSKSSIVGWPIVRERMRRAEPAADGVGAVSRDLEKHGAITSSNIAATNADCAWLEA
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                                                                                                                                             Fang G., Weiser B., Visosky A., Burger H.; "Constructing full-length chimeric HIV-1 molecular clones by mediated recombination.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 206;
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                                                                                                                                                                                                                                                                                                                                                                                                                           9F94AEB9CAFDC6F6 CRC64;
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last sequence update)
Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1119; DB 15;
Pred. No. 2.3e-82;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001558; F-protein.
Pfam: PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23428 MW;
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98.58;
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65AF3B6184DC2FE7 CRC64;

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STRAIN-7-IT
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                                                                       09WM16
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RESULT
Q9WM16
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Kohleisen B., Neumann M., Herrmann R., Brack-Werner R., Krohn K.J.,
Ovod V., Ranki A., Erfle V.;
"Cellular localization of Nef expressed in persistently HIV-1-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FPDWQNYTPGPGIRYPLTFGWCYKLVPVEPDKVEEANEGENTRLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                        61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 231
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AIDS 6:1427-1436(1992).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
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                                                                       Length 206;
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                                                                                                                                               Indels
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01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                       DB 15;
                                                                Score 1115; DB 15
Pred. No. 4.9e-82;
                                                                                                                                       1; Mismatches
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                                                                                                                                               Conservative
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                                                                                                         Similarity
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Best Local S:
Matches 202
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121 LPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular epidemiology study.";
Submitted (Jun.197) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
                                                                                                                                                                                                                                                                                                           Visco Comandini U., Yun. Z., Paganelli R., Orlandi P., Salotti A., Johansson B., Vahlne A., Sonnerborg A.;
"HIV-1 nef mutations and clinical long-term non progression: a molecular epidemiology study.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; LEEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.8%; Score 1105; DB 15; Length 206; llarity 97.1%; Pred. No. 3.1e-81; Conservative 2; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001558; F-protein.
Pfam: PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23333 MW; ZEBF2A6A3ECAF5EA CRC64;
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                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE PACTOR (F-PROTEIN) (27 KDA PROTEIN).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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  PRELIMINARY;
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Best Local Similarity
Matches 200; Conserv
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                                                                                Length 206;
                                                                                                   Indels
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NCE 206 AA; 23439 MW; 8478CF194D39D5B9 CRC64;
                                                 OED69927C2E03BB6 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                              Score 1104; DB 15;
Pred. No. 3.7e-81;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                       206 AA
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                 Interpro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS: GTP-binding; Myristate.
SEQUENCE 206 AA; 23345 WW; (
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InterPro; 1PR001558; F-protein.
EMBL; AF011469; AAD01447.1; -. HSSP; P03406; 1EFN.
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                                                                             48.8%;
ilarity 97.1%;
Conservative
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AIDS 6:1427-1436(1992).
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Best Local Similarity 96.1
Matches 198; Conservative
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01-MAY-2000 (
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Best Local Simil
Matches 200; (
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Pred. No. 1.6e-80;
1; Mismatches 5; Indels 0
                                                                                                                              Created)
Last sequence update)
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(27 KDA PROTEIN).
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Last annotation update)
(27 KDA PROTEIN)
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Retroviridae; Lentivirus
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MEDLINE-95074930; Pubmed-7983770;
Fang H., Pincus S.H.;
Unique insertion sequence and pa
selected with immunotoxins from hinfected T cells.";
LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                       virus
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Best Local Similarity 95.6%;
Matches 197; Conservative
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                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19, NEGATIVE FACTOR (F-PROTEIN)
                                                                                                                                                                                                    Human immunodeficiency vir
Viruses; Retroid viruses;
NCBI_TaxID=11676;
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Fang H., Pincus S.H.;
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3orsetti A.,
'Variability
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                                   SEQUENCE FROM N.A.
MEDLINE-86667228; Pubmed-2999715;
Ratner L., Starcich B., Josephs S.F., Hahn B.H., Reddy E.P.,
Livak K.J., Petteway S.R.Jr., Pearson M.L., Haseltine W.A., Arya S.K.,
Wong-staal F.;
                                                                                                                                                                                                                                                                                                         112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
                                                                                                                             Nucleic Acids Res. 13:8219-8229(1985).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; 1EFN.
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MEDLINE-89352106; PubMed-2765297;
Rederico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.
Macchi B., Mangiano N., Verani P., Rossi G.;
"Biological and molecular characterization of producer and non
producer clones from HUT-78 infected with a patient HIV isolate.";
AIDS Res. Hum. Retroviruses 5:385-396(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Titti F., Federico M:, Butto S., Orecchia A., Carlini F., Taddeo B.
                                                                                 "Polymorphism of the 3' open reading frame of the virus associated with the acquired immune deficiency syndrome, human T-lymphotropic virus type III.";
                                                                                                                                                                                                                                                                                                                                                    Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q., Verani P., Rossi G.B.;
Sequence analysis of HIV-1 proviral DNA from a non producer chronically infected HUT-78 cellular clone.";
J. Viral Diseases 1:40-55(1992).
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                                                                                                                                                                                                                                                          Score 1096; DB 15; Length 206; Pred. No. 1.6e-80; 4; Mismatches 3; Indels 0
                                                                                                                                                                                                                         3B25EB332A479A46 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
Viruses; Retroid viruses; Retroviridae.
NCBL_TaxID=11966;
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                                                                                                                                                                                             Pfan, PF00469; F-protein; 1. AIDS, GTP-binding; Myristate. SEQUENCE 206 AA; 23419 MW;
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Best Local Similarity
Matches 199; Conserv
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-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; PO3406; LEFN.
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP; P03406; 1EFN.
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                          an infected but
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Last sequence update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                              Score 1096; DB 15;
Pred. No. 1.6e-80;
3; Mismatches 4;
Saggio I., Verani P., Rossi G.;
of HIV-1 virus: characteristics of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Pfam; PF00469; F-protein; 1.
ALDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23512 MW;
                                                                                                                                                                                               InterPro: IPR001558; F-protein. Pfam; PF00469; F-protein; 1. AIDS; GTP-binding; Myristate. SEQUENCE 206 AA; 23398 MW;
                                                                                                                                                                                                                                                                                                                                                                 48.4%;
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.6
Matches 199; Conservative
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Matches 197; Conserv
                                                     productive clone."
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23649 MW;
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Q74913;
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Q74913
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- SIMILARITY: NEF HAS GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(14) ANTIGEN.
     231
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                                                                       MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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               121 FPDWQNYTPGPGIRYPLIFGWCXKLVPVEQEKVEEANEGENTRLLHPVSLHGMDDPEREV
    QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                       FPDWONYTPGRGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 FPDWQNYTPGPGVRXPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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Last annotation update)
(27 KDA PROTEIN).
                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1090; DB 15;
Pred. No. 5e-80;
                                                                                                                                                                                                           206 AA
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                                                                                                             LEWRFDSRLAFHHVARELHPEYFKNC
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AIDS; GTP-binding; Myristate.
SEOUENCE 206 AA; 23617 MW;
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01-NOV-1996 (TrEMBLrel. 01, L,
01-DEC-2001 (TrEMBLrel. 19, L,
NEGATIVE FACTOR (F-PROTEIN) (;
NBF.
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95.18;
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Matches 196; Conservative
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Q89561;
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Q89561
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Q74905
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PROUECE FROM N.A.

REQUENCE FROM N.A.

A Arens M.Q., Fatner L., Joseph T., Bandres J.;

A Lens M.Q., Fatner L., Joseph T., Bandres J.;

A Arens M.Q., Fatner L., Joseph T., Bandres J.;

ALTIVITIES, IT SEEMS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR EMBL; U44448; AAB38100.1; -.

DR EMBL; U44447; AAB38109.1; -.

DR HSSP, Q70627; ZNEF.

InterPro; IPR001558; F-protein.

DR Pfam; PF00469; F-protein; I.

KW AIDS; GTP-binding; Myristate.

CFOHENCE 206 AA; 23629 MW; BF467FBIB7147CDE CRC64;
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SEQUENCE FROM N.A.
MEDLINE-96400183: PubMed-8806559;
Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A., Hahn B., Powderly W., Arens M.;
"Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects at different stages of disease.";
Virology 223:245-250(1996).
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EMBL: U44453; AAB38205.1; -.
Interpro Troop
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                                                                                                                                                                                                                                                                                                                                                       Score 1087; DB 15; Length
Pred. No. 8.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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Last sequence update)
Last annotation update)
(27 KDA PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                   Query Match 48.0%; Score 1087; D
Best Local Similarity 94.7%; Pred. No. 8.7e
Matches 195; Conservative 7; Mismatches
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MEDLINE-96400183; PubMed-8806559;
Ratner L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A., Hahn B., Powderly W., Arens M.;
"Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects at different stages of disease.";
Virology 223:245-250(1996).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTQGY 120
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                                                                                                                                                                                                                                                                                                                                            ACTIVITIES, IT SEENS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL; U44454, AAB38206.1; -. The CD4 (T4) ANTIGEN.
HSSP; P03406; 1EFN.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
                              Last annotation update) (27 KDA PROTEIN).
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                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 1079; DB 15;
95.1%; Pred. No. 3.8e-79;
Live 5; Mismatches 5;
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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Pfam; PF00469; F-protein; 1.
AIDS: GTP-binding; Myxistate.
SEQUENCE 206 AA, 23615 MW;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
  01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                NEGATIVE FACTOR (F-PROTEIN)
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Matches 195; Conserv
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- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITEES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN. HSSP; P03406; 1EFN.
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                                                                                                                                                                                                                         112 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 171
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                            1 MGGKWSKSSVIGWPTVRERWRRAEPAADGVGAVSRDLEKHGAITSSVIAATNADCAWLEA
                                                                                                 172 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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47.7%; Score 1080; DB 15; Length 206;
Best Local Similarity 94.7%; Pred. No. 3.2e-79;
Matches 195; Conservative 5; Mismatches 6; Indels 0
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(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23362 MW;
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MEDLINE-96400183; PubMed-8806559;
Mather L., Joseph T., Bandres J., Ghosh S., Heyden N.V., Templeton A., Hahn B., Powderly W., Arens M.;
Sequence heterogeneity of Nef transcripts in HIV-1-infected subjects at different stages of disease.";
virology 223:245-250(1996).
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                                                 Gaps
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                            Length 206;
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Pfam, PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23488 MW; F0596D6FAAA81A05 CRC64;
 E5BD6FA0B70FC175 CRC64;
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Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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llarity 94.2%; Pred. No. 5.6e-79;
Conservative 7; Mismatches 5;
                          Ouery Match
47.7%; Score 1079; DB 15;
Best Local Similarity 95.6%; Pred. No. 3.8e-79;
Matches 195; Conservative 5; Mismatches 4;
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 23648 MW;
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Matches 194; Conserv
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TEATIVE TILES.

TO Piedade J., Esteves A., Parreira R., Venenno T., Barros M.F.,

RA Canas Ferreira W.F.,

Consider and expression of HIV-1 nef gene in the carrier-adjuvant

RT Cloning and expression of HIV-1 nef gene in the carrier-adjuvant

RT PVUB3 expression system based on the major lipoprotein (OprI) from the

RT Outer membrane of Pseudomonas aeruginosa.";

Submitted (JUL-1999) to the EMBL/Genbark/Doby databases

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

CC ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.

DR EMBL. APIG611; AAD47831.1;

DR HSSP; PO3406; IEFN.

InterPro; IPRO01558; F-protein.

DR Pfam; PR00465; F-protein.

RW AIDS; GTP-binding; Myristate.

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"HIV-1 Strains from a cohort of American subjects reveal the presence
of a V2 region extension unique to slow progressors and non-
progressors.";
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                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN) (FRAGMENT).
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(27 KDA PROTEIN).
                                                                                                                                             Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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202 AA.
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0; Mismatches
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Best Local Similarity 97.5%;
Matches 197; Conservative
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181 KVLEWRFDSRLAFHHVARELHPEYFKNC 208
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                                                      LEWRFDSRLAFHHVARELHPEYFKNC
                                          292 LEWRFDSRLAFHHVARELHPEYFKNC
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Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang B., Saksena N.K.; "HIV-1 Strains from a cohort of American subjects reveal the of a V2 region extension unique to slow progressors and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1072; DB 15; Length 206; Pred. No. 1.4e-78; 5; Mismatches 8; Indels 0
                                                                                                                Score 1072; DB 15; Length 206;
Pred. No. 1.4e-78;
2; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A66FC8B78FFECFD2 CRC64;
                                                                                    081DF3A12E5A7576 CRC64;
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Last annotation update)
(27 KDA PROTEIN),
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                       1.4e-78;
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                                                                                                                                                                                                                                                                                             292 LEWRFDSRLAFHHVARELHPEYFKNC 317
                                                  InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 25310 MW;
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AIDS: GTP-binding; Myristate, eronrewre 206 AA; 23420 MW;
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Local Similarity 93.7%;
les 193; Conservative
                                                                                                                  Query Match
Best Local Similarity 94.7%;
Matches 195; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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AIDS 0:0-0(2000).
AIDS 0:0-0(2000)
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61 EAQEEEEVGFPVTPQVPLRPMTXKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johansson B., Vahlne A., Sonnerborg A.;
"HIV-1 nef mutations and clinical long-term non progression: a molecular epidemiology study.";
Submitted (JNN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
BNBL; AF011470; AAD01448.1; -.
HSSP; P03406; 1EFN.
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AIDS; GTP-binding; Myristate.
SEQUENCE 208 AA; 23681 MW; 1C891C3AD230C6A8 CRC64;
                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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94.2%; Pred. No. 1.7e-78;
11ve 3; Mismatches 7;
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MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                    QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                            232 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA, 23514 MW;
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ilarity 91.7%;
Conservative 1:
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                                                                                                                                                                             -1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4 (T4) ANTIGEN. EMBL; PG04465; AAC18377.1; -. EMBL; PG04465; LEW. INTERPRO; IPRO01558; F-protein.
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AIDS Res. Hum. Retroviruses 16:1855-1868(2000).
-1- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP: P03406; leen.
SEQUENCE FROM N.A.
STRAIN-PATIENT 27;
STRAIN-PATIENT 27;
STRAIN-PATIENT 27;
Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system of H positive individuals/AIDS patients with or without AIDS dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21002575; PubMed-11118071; Geffin R., Wolf D., Muller R., Hill M.D., Stellwag E., Freitag M., Sass G., Scott G.B., Baur A.S.; "Functional and structural defects in HIV-1 nef genes derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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                                                                                                                                                                                                                                                                                                                                              DEE21CAF05891D6B CRC64;
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.2%; Score 1068; DB 15; Best Local Similarity 91.7%; Pred. No. 3e-78; Matches 189; Conservative 14; Mismatches 3;
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SEQUENCE 206 AA; 23464 MW;
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09DQU1
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291
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EMBL; AF064675; AAC18375.1; --
HSSP; P03406; 1EFN.
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STRAIN-PATIENT 27;
MCPHee D.A., Greenway A.L., Holloway G., Smith K., Deacon N.,
Pemberton L., Brew B.J.;
"Anomalies in Nef expression within the central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 206;
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01-NOV-1999 (TREMBLrel. 12, Last sequence update),
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN)
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; Pred. No. 6.2e-78;
13; Mismatches 4;
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DOWN-REGULATE THE CD4(T4) ANTIGEN
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"HIV-1 Strains from a cohort of
of a V2 region extension unique
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                                     InterPro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23472 MW;
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ilarity 92.7%;
Conservative
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IT SEEMS TO
AAC18374.1;
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Matches 189; Conserv
            EMBL; AF064673; AAC
HSSP; P03406; 1EFN
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Best Local Simi
Matches 191;
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090597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 17:58-68(1998).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
EMBL, AF063922; AAC17893.1; -.
HSSP; PO3406; 1EFN.
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Pandaalies in Nef expression within the central nervous system of I positive individuals/AIDS patients with or without AIDS dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPGREV
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                                                                                                                                                                                Kang M.R., Cho Y.K., Chun J., Kim Y.B., Lee I., Lee H.J., Kim S.I. Kim Y.K., Yoon K., Yang J.M., Kim J.M., Shin Y.O., Kang C., Lee Ghoi K.W., Kim D.G., Fitch W.M., Kim S., Fin Y.O., Kang C., Lee "Phylogenetic analysis of the nef gene reveals a distinctive monophyletic clade in Korean HIV-1 cases.";
                                                                                                                                                                                                                                                                                                                                                                                                  Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                            4D5AEDF55FAE93E3 CRC64;
                                     Last sequence update)
Last annotation update)
(27 KDA PROTEIN).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 1062; DB 15;
llarity 94.6%; Pred. No. 9e-78;
Conservative 3; Mismatches 8;
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206
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                                                                                                                                                         STRAIN-PATIENT 9;
MEDLINE-98097260; Pubmed-9436760;
                                                                                                                                                                                                                                                                                                                 Interpro; IPR001558; F-protein.
Pfam; PF00469; F-protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23348 MW;
                                                                NEGATIVE FACTOR (F-PROTEIN)
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PRELIMINARY;
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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American subjects reveal the presence to slow progressors and non-
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2255A447ECE85456 CRC64;
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Last annotation update)
(27 KDA PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                       46.9%; Score 1061; DB 15;
91.7%; Pred. No. 1.1e-77;
live 12; Mismatches 5;
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Pred. No. 1.3e-77;
7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 FPDWONYTPGPGIRYPLTFGWCYKLVPVEQEKVKKANEGKNTSLLHPMSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                                                                          J. Neurovirol. 4:0-0(1998).
-!- SIMILARITY: NEF HAS GTPASE, GTP-BINDING AND AUTOPHOSPHORYLATING ACTIVITIES, IT SEEMS TO DOWN-REGULATE THE CD4(T4) ANTIGEN.
HSSP: P03406; 1EFN.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NEGATIVE FACTOR (F-PROTEIN) (27 KDA PROTEIN).
                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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46.7%; Score 1057; DB 15;
Best Local Similarity 91.3%; Pred. No. 2.3e-77;
Matches 188; Conservative 13; Mismatches 5;
                                                                                                                           206 AA.
                                          191 LEWRFDSRLAFHHVARELHPEYFKNC 206
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                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00469; F-Protein; 1.
AIDS; GTP-binding; Myristate.
SEQUENCE 206 AA; 23442 MW;
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Amino acid sequenc Lyst I mutant tat a HIV virus recombin Tat protein derive cDNA for tat protein Sequence of the HIV TAT. Human immunodefici HIV tat protein.

Amino acid sequence HIV Type I TAT protein.

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Amino acid seque Lys41 mutant tat HIV virus recombil Tat protein derii	CDNA for tat pro Synthetic TAT pro Sequence of the HIV TAT. Human	-1 or ⊟ or or	TAT Protein. Sy Cys22 mutant tat Sequence of the Wild type TAT HI	RGD-delta mutant Wild type Tat am	Diversified HIV- Peptide fragment HIV-1 tat protei	Full length TAT. Human protein: S HIV-1 Tat peptid HIV-1 Tat peptid	Trans-dominant v HV Tat_SF162. HV Tat_Cy32_SF HIV-1 strain OYI Sequence of the Trans-acting tran					protein; Tat protein;								
536 97.1 413 22 479 86.8 86 20 478 86.6 86 8 478 86.6 86 10	478 86.6 86 10 478 86.6 86 10 478 86.6 86 14 478 86.6 86 17 478 86.6 86 17	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	4/6 00.0 0/12 466 84.4 86 20 462 83.7 86 11 462 83.7 86 16 467 5 82 93 20	1 456.5 82.7 83 20 AAY2295 2 452 81.9 83 20 AAY2295	451 81.7 86 15 451 81.7 86 15 448 81.2 86 21	6 446 80.8 86 7 446 80.8 86 8 442 80.1 86 9 442 80.1 86	433 78.4 86 16 AAR7754 430 77.9 101 21 AAB1422 418 75.7 102 21 AAB1422 411 74.5 101 12 AAR1225 411 74.5 101 21 AAB3051 408 73.9 72 7 AAB60699	ALIGNMENTS	RESULT 1 AAY02356 ID AAY02356 standard; Protein; 95 AA.	XX AC AAY02356; XX DT 09-JUL-1999 (first entrv)	A representat	HIV nef gene; fusion protein; HIV nef gene; Nef vaccine; HIV infection; protein D.	S Synthetic. S Human immunodeficiency virus type 1. N W09916884-A1.	X D 08-APR-1999.	17-SEP-1998;	K 26-SEF-1997; 9/GB-UU2U383. X A (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.	A Bruck C, Godart SAG, Marchand M;	A. WPI; 1999-302282/25. DR N-PSDB; AAX35692.	XX PT HIV Tat or Nef protein linked to a fusion partner	X S Disclosure; Fig 2; 66pp; English.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Comp	search, using sw model ist 26, 2002, 08:12:30 ;	106 US-09-509-239-23 552 1 MEPVDPRLEPWKHPGSQPKT	BLOSUM62 Gapop 10.0 , Gapext 0.5 747574 secs, 111073796 residues	satisfying chosen p	length: 0 length: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_032802:*  1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*  2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*  3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*  4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*  5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*	/SIDS1/gcgdata/hold-geneseq/g /SIDS1/gcgdata/hold-geneseq/g /SIDS1/gcgdata/hold-geneseq/g	/SIDS1/gcgdata/hold-geneseq/e :/SIDS1/gcgdata/hold-geneseq/e :/SIDS1/gcgdata/hold-geneseq/e	/31D31/gcgdata/hold-genesed/ /S1D51/gcgdata/hold-geneseq/ /S1D51/gcgdata/hold-geneseq/ /S1D51/gcgdata/hold-geneseq	<pre> /SIDS1/gcgdata/hold-geneseq, /SIDS1/gcgdata/hold-geneseq, /GIDS1/gcgdata/hold-geneseq,</pre>	/SIDS1/959data/hold-geneseq, /SIDS1/959data/hold-geneseq, /SIDS1/959data/hold-geneseq, /SIDS1/959data/hold-geneseq,	No. is the number of results predicted by chance to greater than or equal to the score of the result bederived by analysis of the total score distribution	SUMMARIES	، د د ده	!	302 22	302 20	411 20	413 20
ū	OM protein - protein Run on: Augu	Title: US Perfect score: 55 Sequence: 1	Scoring table: BI Garched: 74	mber of h	Minimum DB seq lend Maximum DB seq lend	Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Database : 1:			14 14 15	17	20 20 21 21 22 22 22 22	Pred. No. is score greated and is derive	đ	Result Quo	552 552 547	547	7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	23 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	536

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         The present sequence represents a representative HIV-I mutant Nef-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-I Tat protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                                                                                                   Gaps
                                                                                                                                                                                      New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine
                                                                                                                                                                          1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ
                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a His-tagged mutant Tat protein of HIV
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                                                                                                                              95;
                                                                                                                              Length
                                                                                                                                                     Indels
                                                                                                                          ; Score 552; DB 20;
; Pred. No. 3.4e-50;
0; Mismatches 0;
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                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                        AAG63238 standard; Protein; 95
                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 95; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus
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2000GB-0009336.
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28-JUN-2000; 2000WO-EP05998
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N-PSDB; AAH42882.
                                                                                          95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200154719-A2
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14-APR-2000;
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                                                                    infection.
                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                            Sequence
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The present sequence represents a representative HIV-1 mutant Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; fusion protein; HIV nef gene; Nef protein; Tat protein; HIV infection; protein D.
                                             Gaps
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                                                                                                             1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ
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  Length 95;
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.1%; Score 547; DB 20;
100.0%; Pred. No. 3.8e-49;
iive 0; Mismatches 0;
100.0%; Score 552; DB 22;
100.0%; Pred. No. 3.4e-50;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A representative HIV-1 mutant Tat-His protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                  AAY02357 standard; Protein; 302
Query Match
Best Local Similarity 100.
Matches 95; Conservative
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ses 94; Conservative
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N-PSDB; AAX35693.
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AAG63239

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The present sequence represents a representative HIV-1 Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                               protein; HIV nef gene; Nef protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; nef gene; tat gene; vaccine; gpl20 gene; HIV viral load
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 541; DB 20;
Pred. No. 4.8e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                               A representative HIV-1 Tat-His protein.
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                                                                                                                                                  Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                               Marchand M;
                                                                                                 HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG63232 standard; Protein; 95 AA.
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              (first entry)
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N-PSDB; AAX35686.
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Best Local Similarity
Matches 92; Conserv
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            09-JUL-1999
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                                                                                                   vaccine;
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                                                                                 HIV nef
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine
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                                                                                                                                                                   Amino acid sequence of a His-tagged mutant His protein of HIV.
                                                                                                                                                                                                     HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                               Protein; 302 AA.
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                                                                                                                                                                                                                                                        Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                              2000GB-0009336.
2000GB-0013806.
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                                                                                                                                (first entry)
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                                                               standard;
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06-JUN-2000;
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Voss G;

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29-JAN-2001; 2001WO-EP00944.

AAY02350

AAY02350 ID AAY0: XX AC AAY0:

RESULT

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Length 95; Indels

Gaps

Joss G;

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The present sequence represents a His-tagged Nef-Tat linked protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or
                                                                                                                                      The present sequence represents a representative HIV-1 Nef-Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The fusion protein can be used in a vaccine to prevent HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of a His-tagged Nef-Tat linked protein of HIV.
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                                                                   HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                   Score 536; DB 20;
Pred. No. 5.3e-48;
2; Mismatches 1;
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                                                                                                      Disclosure; Fig 2; 66pp; English.
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2000GB-0009336.
2000GB-0013806.
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96.8%;
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               WPI; 1999-302282/25
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                     AA;
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                            N-PSDB; AAX35687
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06-JUN-2000;
28-JUN-2000;
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AAG63233
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                                                                                                                                                                                                                             New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 541; DB 22; Length 95;
Pred. No. 4.8e-49;
2; Mismatches 1; Indels
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                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 90pp; English
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           2000GB-0002200.
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2000GB-0013806.
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96.8%;
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Best Local Similarity 96.8
Matches 92; Conservative
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           31-JAN-2000;
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06-JUN-2000;
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                                                                     28-JUN-2000;
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Seguence

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vaccine;

Bruck C,

SQTHQVSLSKQPTSQSKGEPTGPKETSGHHHHHH

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  Nef-Tat act
therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; Nef protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQG
                                                                                                                          EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 Nef protein. The fusion protein can be used in prevent HIV infection.
                                                                                   Score 536; DB 22; Length 302;
Pred. No. 5.3e-48;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.1%; Score 536; DB 20;
96.8%; Pred. No. 7.3e-48;
ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                       A representative LipoD-Tat-His fusion protein.
                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                         HIV nef gene; fusion protein; HIV nef vaccine; HIV infection; protein D.
                                                                                                                                                                                                                                                                                                                                     Synthetic.
Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 66pp; English.
                                                                                                                                                                                                                               AAY02353 standard; Protein; 411
                                                                                   97.1%;
ilarity 96.8%;
Conservative 2
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Best Local Similarity
Matches 91; Conserv
                                                                                    Query Match
Best Local Similarity
Matches 91; Conserv
                                                         302 AA;
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                                                           Sequence
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The present sequence represents a His-tagged Nef-Tat linked protein of HIV, with a lipidation signal sequence (Lipob) which is removed after processing and a Proto fusion partner. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV ppi20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV The vaccine reduces the HIV viral load in HIV in the vaccine is a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a His tagged LipD-Nef-Tat linked protein.
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                                                                                                                                                                                                                                                                                                                                                                       HIV; nef gene; tat gene; vaccine; gpl20 gene; HIV viral load
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96.8%; Pred. No. 7.3e-48;
Live 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "ProtD fusion partner"
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                         AAG63235 standard; Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0002200.
2000GB-0009336.
2000GB-0013806.
2000WO-EP05998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus.
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Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH42879.
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14-APR-2000;
06-JUN-2000;
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                                                                                                                                                                                                                                                                  01-OCT-2001
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Peptide
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Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                          413 AA;
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                                                              WO200154719-A2
                                                                                                            31-JAN-2000;
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06-JUN-2000;
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         Synthetic
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                                                                                                                                                                                                                                                                                                                                            Sequence
                                       Peptide
                                                                                                                                                                   Voss G;
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                                                                                                                                                                                                                                                                                                                                                                                                                               nef gene; Nef protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a His tagged ProtD-Nef-Tat fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; nef gene; tat gene; vaccine; gpl20 gene; HIV viral load
                                                                                                                                                                                                                                                                                                                                                                                          Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                    or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                                                        Score 536; DB 20;
Pred. No. 7.3e-48;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQTHQVSLSKQPTSQSKGEPTGPKETSGHHHHHH 95
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                                                                                                    A representative LipoD-Tat fusion protein.
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                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG63237 standard; Protein; 413 AA
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                                                                                                                                         Synthetic.
Human immunodeficiency virus type
                                                                                                                   gene; fusion protein; HIV : HIV infection; protein D.
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                                                     AAY02355 standard; Protein; 413
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96.8%;
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                                                                                                                                                                                                                                               Godart SAG,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  413
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                                                                                    09-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                         91;
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                                                                                                                                                                                                                                               Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG63237;
                                                                                                                  HIV nef g
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                    AAY02355;
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                                              AAY02355
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The present sequence represents a His-tagged ProtD-Nef-Tat fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the luvention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylabacisc or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gp120 protein or polynucleotide for the manufacture of a vaccine -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 413;
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Pred. No. 7.3e-48;
2; Mismatches 1;
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                                                                                              1..111
/note= "ProtD fusion partner"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                               Location/Qualifiers
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96.8%;
Human immunodeficiency virus
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2000GB-0013806,
2000WO-EP05998,
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Wong-Staal F;

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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence encoding this protein is present in E. coll plasmids pAS1, pOTS-tatillD or pOTS-tatill. Recombinant tat-3 protein and its derivatives can be used in the detection and therapy of HIV virus infection as well as an an antigenic component of a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tat protein cDNA; HTLV-III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tat protein derived from human immuno-deficiency virus (HIV: HTLV-III/LAV) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes the HIV virus tat-3 protein.

    has protein coding complementary DNA from human
immuno:deficiency virus in genome DNA domain

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Pred. No. 1.6e-42;
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                                                                                                             Rosenberg C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 gsqthqvslskqptsqsrgdptgpke 86
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                            (SMIK ) SMITHKLINE BECKMAN CORP. (USDC ) US DEPT COMMERCE.
                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 14; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant vaccinia virus; HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.6%;
96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                             Aldovinni A, Debouck CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.5
Matches 83; Conservative
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N-PSDB; AAN92430.
                                                                                                                                                               WPI; 1987-150612/21.
N-PSDB; AAN70948.
                                                                                                                                                                                                                                                                                                   HTLV-III infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAV; AIDS; ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP01085072-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP91903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents tat protein. The specification describes for the use of biologically active HIV Tat protein, fragments or mutants for the prophylactic or therapeutic treatment of AIDS and tumours, syndromes and symptoms associated with HIV infection. A biologically active Tat protein, fragments and/or mutants and/or Tat DNA which is capable of entering and localizing in the nuclei of activated endothelial cells or dendritic cells and/or activating the proliferation, migration and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated endothelial cells, is used as a vaccine. HIV-1 Tat or its mutants in a bhologically active form is able to induce a very strong immune response against HIV, able to prevent infection or the development of the disease and to permit efficient therapeutic strategies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of biologically active HIV Tat protein, fragments or mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV virus; tat-3 protein; plasmid pAS1; plasmid pOTS-tatIIID; plasmid pOTS-tatIII; AIDS; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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Pred. No. 1.3e-42;
2; Mismatches 1;
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV virus recombinant tat-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 117; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.8%;
96.5%;
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nes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-385324/32,
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX81356
                                                                                                                                                          30-NOV-1998;
                                                                                                                                                                                                                  01-DEC-1997;
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                                                                                                    10-JUN-1999
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Matches
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Gaps

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The DNA

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It is inserted into the genome of vaccinia viruses in a region which is not essential for their propagation to create recombinant vaccinia viruses. These viruses are propagated in animal cells together with recombinant vaccinia viruses which contain DNA coding for a useful protein, for example, human growth hormone, insulin, interferons, interferors amylase, protesse. The presence of tat protein assists the mass-production of the useful protein.
                                                                                                                                                                 ö
All or part of it can be produced by recombinant vaccinia virus by integrating it into the genome region nonessential for vaccinia virus proliferation and then infecting animal cells with the recombinant virus. Tat protein can be used to diagnose HIV infection and for prophylaxis for AIDS or ARC patients. It can also be used to develop a live vaccine using temperature-sensitive Lister strain of vaccinia virus.
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA for tat protein of human immunodeficiency virus (HIV).
                                                                                                                                       Length 86;
                                                                                                                                    Score 478; DB 10; Length 8 Pred. No. 1.6e-42; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using recombinant vaccinia viruses contg. protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccinia virus
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46..306
/*tag= a
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                                                                                                                                                                                                                                                                                                                                            AAP91905 standard; protein; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV; recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus
                                                                                                                                    Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        tat protein;
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Length 86;

DB 10;

86.6%; Score 478;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                        protein; HIV-1; tat gene; trans-activator; anti-terminator;
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                                                                                                                                                                                                                                                                                                                                                                                            Synthesis of double stranded DNA, esp. TAT gene of HIV - by contg. a single and double stranded portion and in vivo gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
  Pred. No. 1.6e-42; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 478; DB 10;
Pred, No. 1.6e-42;
2; Mismatches 1;
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                                                                    AA.
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                                                                                                                                          98
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Best Local Similarity 96.5%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                    89WO-GB00384.
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  96.5%;
                                                                                                                                          protein;
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           Conservative
                                                                                                                                                                                                                                                                                                                                              Adams SE;
                                                                                                                                                                                                     Synthetic TAT protein
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-324229/44.
                                                                                                                                         AAP93140 standard;
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA;
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                                                                                                                                                                                                                                                                                    14-APR-1989;
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                                                                                                                                                                                 21-MAR-1990
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                                                                                                                                                              AAP93140;
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                                                                                                                                  AAP93140
                                                                                                                      RESULT
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Domain Region

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This sequence represents the HIV transactivating protein, TAT. The sequences given in AAR86601-19 are immunogens derived from the cellular uptake region of this protein. These peptides are based on the region comprising amino acids 46-63. The immunogenic peptides are used to protect against infection by HIV. They may also be used to reduce viraemia in already infected patients. These immunogens may be used to identify, or generate, antibodies specific for TAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
   Immunogen; cellular uptake region; transactivating protein; TAT; HIV;
vIraemia; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogen containing cellular uptake region of viral TAT protein -induces high antibody titre against TAT, partic. for preventing or treating HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 1.6e-42;
}; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Immunodeficiency Virus Type 1 Tat protein.
                                                                                                                             /note= "Cellular uptake region"
                                                                                                                                                                                                                                                                                                                                                    Shenbagamurthi P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22..36
/label= cysteine_rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Figure 1; 54pp; English.
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                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                (IMMU-) IMMUNOGIOLOGY RES INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.68;
96.58;
                                                       Human immunodeficiency virus
                                                                                                                                                                                                                                                                            94US-0247991
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                                                                                                                                                                                                                                                                                                                                                    Goldstein G,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-049298/05.
N-PSDB; AAT06634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AA;
                                                                                                                                                                                                                                                                            23-MAY-1994;
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                                                                                                                                                                                                       30-NOV-1995
                                                                                                                                                                                                                                                                                                                                                    Culler MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                             Key
Peptide
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directed viral gene expression. TAT induced transactivation requires the present of the TAR (transactivation response) element, located at the 5'UTR of the VIRI MRNA element. The sequence of RNA target molecules were chosen based on previous studies characterising the binding properties of the HIV-encoded TAT protein and the TAR target region from both HIV-1 mAINA (nt 1-57). The RNA substrate is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1; HIV-1; TAT protein; transactivator; long terminal repeat; transactivation response element; TAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral polypeptide(s) with site-specific RNA binding - contain molety to cleave RNA backbone and are used to inhibit HIV antigen
                                                                                                                                                                                                                       "proteolytic product of wt TAT protein which binds specifically to TAR-element-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                            Location/Qualifiers
49..57
/label- nuclear targeting domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Figure 2A; 94pp; English.
Sequence of the HIV-1 TAT protein.
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                                                                                                          Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in infected cells
                                                                                                                                                                                                                                                                                                                                                                   92WO-US10770
                                                                                                                                                                                                                                                                                                                                                                                                    91US-0808452
92US-0826934
                                                       long terminal repeat; trans
RNA binding; RNA cleavage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnston BH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 96.5
Matches 83; Conservative
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Sequence

Query Match

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AAR86625

XEXEXEX

HIV TAT

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Region Domain

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This polypeptide comprises the HIV tat protein. Novel transport proteins comprise modified HIV tat covalently attached to a cargo molecule (see AAW26436.42). The modified tat protein (see AAW26444-49) is characterised by the presence of the tat basic region (thought to be required for nuclear localisation), and the absence of the Cys-rich region and the exon 2-encoded C-terminal region. These modifications solve the potential problems of spurious trans-activation and disulphide aggregation, while the reduced size of the transport proteins minimises interference with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA constructs for transporting molecules to cells – encode a fusion protein comprising a modified HIV tat protein and a carboxy-terminal cargo molety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biological activity of the cargo molecule. DNA molecules that encode the modified tat fusion proteins are claimed and can be used to deliver polypeptides or nucleic acids to the cytoplasm
                                       HIV; tat protein; transport protein; cargo delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 478; DB 18;
Pred. No. 1.6e-42;
2; Mismatches 1;
                                                                                                         Location/Qualiflers
23..36
/label- Cys-rich_region
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/label= Basic_region
73..86
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                                                                        Human immunodeficiency virus type 1.
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/label= C-terminal
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91US-0636662.
92US-0934375.
93WO-US07833.
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96.5%;
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Best Local Similarity 96.5'
Matches 83; Conservative
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FAWELL S E.
FRANKEL A.
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   HIV tat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PABO C
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24-NOV-1993;
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02-JAN-19
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the Tat protein from Human Immunodeficiency virus, Type 1 which can be used in a novel method for the delivery of bologically active cargo molecules into the cytoplasm and nuclei of eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-1, HIV-2, SIV) is readily taken up into cells when present extracellularly. By modifying the HIV tat protein i.e. removing the cysteine-rich region and the carboxy-terminal domain and covalently linking the protein to a cargo molecule to form a fusion protein, the problems of spurious trans-activation and disulphide aggregation are radicated. The reduced size of transport polypeptides also minimises interference with the biological activity of the cargo molecule. This is applicable for therapeutic, prophylactic or diagnostic intracellular delivery of small molecules and macromolecules e.g. proteins, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion proteins containing truncated HIV tat sequences - useful intracellular delivery of viral repressor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pepinsky RB
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Pred. No. 1.6e-42;
2; Mismatches 1;
49..57
/label- basic_region
73..86
/label- carboxy_terminal_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example I; Fig 1; 77pp; English
                                                                                                                                                                                            94US-0235403.
89US-0454450.
91US-0636662.
92US-0934375.
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93US-0158015.
95US-0450098.
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Best Local Similarity 96.5%;
Matches 83; Conservative
                                                                                                                                                           89US-0454450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acids and polysaccharides
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                                                                                                                                                                                                                                                                                                                                                                                                         PEPINSKY R B.
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                                                                                                                                                                                                                                                                                                                                                      FAWELL S E.
FRANKEL A.
                                                                                                                                                                                                                                                                                   1993;
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21-DEC-1989;
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24-NOV-1993
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Length 86; 1; Indels

1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60

GSQTHQVSLSKQPTSQSKGEPTGPKE 86

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AAW26443 standard; Protein;

RESULT 21

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16-DEC-1997

AAW26443;

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RESULT

AAW71385

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This sequence represents the human immunodeficiency virus (HIV) Type I active cargo molecules into the cytoplasm and nuclei of cells, for active cargo molecules into the cytoplasm and nuclei of cells, for therapeutic, prophylactic or diagnostic purposes. This is accomplished by the presence of a small basic section of tat transport protein of HIV. This is used as it is this protein which is observed to cause human cells in culture to take up HIV. The method involves the use of a cargo moiety in combination with a transport moiety usually in the form of a culs in culture cargo moiety is a human papillomavirus Ez repressor that retains its biological activity after delivery into a target cell and where the transport moiety is one of following HIV tat protein fragments (a) as 47-58, (b) as 47-62, (c) as 47-62. The protein clay delivery of specific peptides into cells at high concentrations due to use of existing transporters. Previous methods of delivery of include bombardment and transforming, which only allow a fraction of the cell population to be infected and can additionally damage cells as they cause physical opening of the cell walls/membranes to allow entry.
                                                                                                                                                                                             TAT protein; cargo molecule; therapy; diagnosis; transport protein; fusion protein; human papillomavirus E2 repressor; target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV tat-derived transport fusion proteins - used to deliver blological active molecules e.g. peptide(s) or nucleic acids, specifically into cytoplasm or nuclei of cells
                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
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                    AAW76148 standard; protein; 86 AA
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96.5%;
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89US-0454450.
91US-0636662.
93WO-US07833.
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95US-0450236
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Matches 83; Conservative
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                                                                                                                                                  HIV Type I TAT protein.
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                                                                                                       24 - NOV - 1998
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21-DEC-1989;
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25-MAY-1995,
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                                                               AAW76148;
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AAW76148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents Human immunodeficiency virus (HIV) Tat 55. a leaderless protein. A leaderless protein refers to a protein that is found in an extracellular environment, but lacks a canonical leader sequence. The specification describes a method for inhibiting export of a leaderless protein from a cell. The method comprises treating the cell with an agent that inhibits binding between the leaderless protein and a transport molecule. Treatment with the inhibiting agent is specifically used to treat angiogenesis and restenosis, i.e. where expression of FGF-2 is inhibited, and the agent is applied to endothelial or smooth muscle cells. Other applications are treatment of tumours neuroblasstoma), inflammation, cell proliferation, complications of diabetes (e.g. retinopathy), viral, bacterial or fungal infections, polycystic kidney disease and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting export of leaderless protein with agent that inhibits binding to transporter protein - especially for treating angiogenesis and restenois by preventing export of fibroblast growth factor, also methods for identifying leaderless proteins and
                                                                                                                                                                                                                                 HIV Tat 85; leaderless protein; inhibition; export; angiogenesis; restencesis; treatment; tumour; inflammation; cell proliferation; diabetes; retinopathy; infection; polycystic kidney disease; atherosclerosis.
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Pred. No. 1.6e-42;
2; Mismatches 1; Indels
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                                                          AAW71385 standard; Protein; 86 AA.
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96.5%;
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N-PSDB; AAV60345.
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Best Local Similarity
Matches 83; Conserva
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Pepinsky RB;

Pabo C,

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                                                                   1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCF1TAALGISYGRKKRRQRRRPPP 60
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Length 86;
Score 478; DB 19; Length 8
Pred. No. 1.6e-42;
2; Mismatches 1; Indels
                                                                                                       61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting a transport molecule involved in non-endoplasmic reticulum (ER)/Golgi leaderless protein export, comprises contacting test cell extracts or membranes with a fusion protein of a leaderless protein and tags to form a complex of the fusion protein bound to the transport molecule, and detecting the transport molecule in an isolated complex. The leaderless protein is a protein found in the extracellular environment that lacks a canonical leader sequence, interleukin (IL) lapha,or 1-beta, fibroblast growth factor (FGF) io 7, human immondeficiency virus (HIV) tat, platelet-derived endothelial cell growth factor (PD-ECGF), ciliary neutrotrophic factor (CNTF), sciatic nerve growth-promoting activity, vas deferens protein, transglutaminase, L-14 lectin, factor XIIIa, thioredoxin-like protein, transglutaminase. The method is used to detect proteins, complexes of proteins, or parts of a larger complex, that bind to and mediate the transport of leaderless proteins, esponsible for transporting sodium and potassium ions across the cell membrane using ATP as the driving force. Transport molecules detected by the interaction with a larger used in assays to identify inhibitors of the interaction
                                                                                                                                                                                 Human immunodeficiency virus; HIV; Tat 85; transport molecule; golgi; leaderless; endoplasmic reticulum; protein export; detection; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting transport molecules, useful for identifying proteins that mediate leaderless protein export across cell membranes, by contacting cell extracts with a fusion protein of leaderless protein and a tag to form a complex
                                                                                                                                                                                                                                                                                                       /note= "Encoded by AGAA"
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 55-56; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                           /note= "Encoded by GAA"
                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                      ..., Location/Qualifiers Misc-difference 53
                                                                                                                                                 Human immunodeficiency virus Tat 85.
                                   AAY96881 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0030613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0807014
                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florkiewicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-464338/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIBL-) CIBLEX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA53572
                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1998;
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                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                              US6083706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baird A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                        AAY96881;
24
             AAY96881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-idiotypic antibodies consisting of one or both amino acid sequences corresponding to amino acid positions 79-84 or 326-400 of processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cher M;
Muster T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                           HIV-1; gp120; BH10; vaccine; immunization; tat protein.
                                                                                                                                                                                                                                                                                  Amino acid sequence of HIV-1 isolate BH10 tat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchacher A, Ernst W, Ballaun C, Purts
edl R, Schmatz C, Klima A, Steindl F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 478; DB 22;
Pred. No. 1.6e-42;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Columns 31-32; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                        type 1.
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86
                        AA.
61 GSQTHQVSLSKQPTSQSKGEPTGPKE
                                                                                                                                                   AAB85996 standard; Protein; 86
                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus
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96.5%;
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                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H, Buc...
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N-PSDB; AAH76385.
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                         30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                              US6268484-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1995;
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Trkola A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections
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                                                                                                                                                                                         AAB85996;
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                                           61
                                                                                                          RESULT 2
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Score 478; DB 21; Length 86; Pred. No. 1.6e-42; 2; Mismatches 1; Indels

Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative

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The present sequence represents tat protein. The specification describes the use of biologically active HIV Tat protein, fragments or mutants for the prophylactic or therapeutic treatment of AIDS and tumours, syndromes and symptoms associated with HIV infection. A biologically active Tat protein, fragments and/or mutants and/or Tat DNA which is eapable of entering and localizing in the nuclei of activated endothelial cells or dendritic cells and/or activating the proliferation, migration and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated endothelial cells, is used as a vaccine. HIV-1 Tat or its mutants in a biologically active form is able to induce a very strong immune response against HIV, able to prevent infection or the development of HIV-1-infected individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of biologically active HIV Tat protein, fragments or mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of the transactivating protein (tat-86) of human immmunodeficiency virus (HIV) (BRU isolate).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.4%; Score 466; DB 20; Length 8 95.3%; Pred. No. 2.9e-41; 1ve 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.72
/note="tentative functional region IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV BRU isolate; transactivating protein; tat-86;
viral replication antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 .48
/note="tentative functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49..57
/note="tentative functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus (BRU isolate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR02227 standard; protein; 86 AA
                                                                                                              SUPERIORE DI SANITA.
                                              98WO-EP07721
                                                                                                                                                                                                                                                              Claim 10; Page 117; 150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                               WPI; 1999-385324/32.
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Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRU isolate;
                                                                                                                                                                                              N-PSDB; AAX81355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                               (SUPE-) INST
                                              30-NOV-1998;
                                                                               01-DEC-1997;
               10-JUN-1999
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The TAT protein here is encoded by the synthetic tat gene but is identical to the TAT protein found in HIV. The expresson of the TAT protein in transformed yeast enables TAT inhibitory agents to be screened to obtain potential anti-viral agents esp. anti-HIV therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene expression system for yeast cells - with TAT protein mediated expression under the control of a HIV regulatory control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV Tat protein; AIDS; tumour; HIV infection; dendritic cell;
Kaposi's sarcoma cell; activated endothelial cell;
cytokine-activated endothelial cell; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 86.6%; Score 478; DB 12; Length 87; Local Similarity 96.5%; Pred. No. 1.6e-42; les 83; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cys22 mutant tat amino acid sequence of HIV-1.
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            87 AA
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          AAR13379 standard; Protein;
                                                                                                                                                                                                                                                                            91EP-0300903
                                                                                                                                                                                                                                                                                                           90GB-0003010
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                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                              Ernst JF,
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-240122/33.
N-PSDB; AAQ13188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AA;
                                                                                                                                                                                                                                                                            04-FEB-1991;
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                                                                           23-OCT-1991
                                                                                                            TAT protein
                                                                                                                                                                                                           EP441582-A.
                                                                                                                                                                             Synthetic.
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Best Local Si
Matches 83;
                                                                                                                                             HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                            Dykes CW,
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                                            AAR13379;
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present sequence represents tat protein. The specification describes use of biologically active HIV Tat protein, fragments or mutants the prophylactic or therapeutic treatment of AIDS and tumours,
                                                                                                                                                                                  immunodeficiency virus) TAT protein. An antiviral compsn. comprising a first trans-dominant variant (esp. derived from HIV TAT; see ARR77542) of a viral protein and a second trans-dominant variant of a different viral protein of the same virus (esp. derived from HIV REV; see AAR78743 and AAR77543) are used to treat or prevent viral infection, esp. HIV. The trans-dominant variant viral proteins inhibit both infection of cells and viral propagation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRORRRPPQ 60
                                                               Compsn. contg. two trans-dominant variants of viral proteins - esp. of TAT and REV HIV proteins, useful for preventing or treating viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of biologically active HIV Tat protein, fragments or mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; dendritic cell; cell;
                                                                                                                                                                      The protein is that of residues 1 to 86 of the HIV (human
                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                              Score 462; DB 16; Length
Pred. No. 7.5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lys41-RGD-delta mutant tat amino acid sequence of HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV Tat protein; AIDS; tumour; HIV infection; Kaposi's sarcoma cell; activated endothelial cytokine-activated endothelial cell; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                     Disclosure; Page 18-19; 31pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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93.0%;
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N-PSDB; AAX81358.
 Sorg T,
                                WPI; 1995-217532/29
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                             86 AA;
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 Mehtali M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensoli B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY22962;
                                                                                                                                                                                                                                                                                                                             Sequence
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for
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                                                                                                                                                                                                                                                                                                                                                                                             The invention provides for a method of preparing peptide antagonists of viral transactivating proteins (TAPs) by producing peptide fragments of the TAP and then selecting those which show antagonistic activity.

Alternatively, peptides contg. an active domain of TAP (or the full length protein) are prepd., and one or more AA substn(s). is made to eliminate transactivating activity without destroying binding ability. The antagonists are useful as therapeutic agents in the control of viral infection and viral pathogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REV; HIV; human immunodeficiency virus; trans-dominant variant; t; prevent; viral infection; viral propagation; inhibit.
                                                                                                                                                                                                                                                                                             New antagonists of viral, esp. HIV, replication - are fragments of trans-activating protein, opt. contg. aminoacid
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73..86
/note="tentative function region V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 462; DB 11;
llarity 93.0%; Pred. No. 7.5e-41;
Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wild type TAT HIV protein (residues 1 to 86).
                                                                                                                                                     89US-0352688, US-207393.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus
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                                                                                                                     89WO-US02404
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                                                                                                                                                                                        (USYL-) ST LOUIS UNIV.
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                                                                                                                                                                                                                                                           WPI; 1990-022386/03
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                     01-JUN-1989;
                                                                                                                                                                                                                                                                                                                             substitution
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                                                  WO8912461-A
                                                                                    28-DEC-1989
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us-09-509-239-23.rag

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syndromes and symptoms associated with HIV infection. A biologically active Tat protein, fragments and/or mutants and/or Tat DNA which is capable of entering and localizing in the nuclei of activated endothelial cells or dendritic cells and/or activating the proliferation, migration and invasion of Kaposi's sarcoma (KS) cells and cytokine-activated endothelial cells, is used as a vaccine. HIV-1 Tat or its mutants in a biologically active form is able to induce a very strong immune response against HIV, able to prevent infection or the development of the disease and to permit efficient therapeutic strategies in
        88888888888888888
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83° AA; Sequence

Gaps Query Match
82.9%; Score 457.5; DB 20; Length 83;
Best Local Similarity 95.3%; Pred. No. 2.1e-40;
Matches 82; Conservative 0; Mismatches 1; Indels 3

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Search completed: August 26, 2002, 08:12:31 Job time: 240 sec

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APPLICANT: FRANKEL, Alan
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDEC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
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US-08-450-098-7
US-08-450-233-7
US-08-450-236-7
US-08-235-403-7
US-08-235-403-7
US-08-50-257-2
US-08-450-246-2
US-08-450-235-2
US-08-450-236-2
US-08-235-2
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US-08-450-257-60
US-08-450-246-60
US-08-450-098-60
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APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/450,257
CLASSIFICATION:
514
PRIOR APPLICATION:
514
PRIOR APPLICATION:
514
PRIOR APPLICATION:
514
APPLICATION NUMBER: US 08/235,403
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/98,766
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/516,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY,AGENT INPORMATION:
NAME: Haley JT., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08450257
Patent No. 5652122
GENERAL INFORMATION:
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60.334 Million cell updates/sec
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552
1 MEPVDPRLEPWKHPGSQPKT.......OSKGEPTGPKETSGHHHHHH 95
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-099-333-1
US-09-030-613-17
US-09-451-905-17
US-08-893-853-1
US-08-094-128A-27
US-08-455-674-27
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US-08-451-233-1
US-08-450-238-1
US-08-450-236-1
US-09-030-613-19
US-09-124-900-6
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US-08-235-403-19
US-08-235-403-1
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US-07-910-867B-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw mode]
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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FILING DATE: 24-NOV-1993 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                              ; STRAIN: type 1
US-08-450-246-1
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US-08-450-098-1
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                                                                                                                                                                                                                                                   Length 86;
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APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INFORTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                               86.6%; Score 478; DB 1;
96.5%; Pred. No. 5.4e-46;
11ve 2; Mismatches 1;
                                                                                                                                                    ORGANISM: human immunodeficiency virus
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FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27,794
ER: B170 CIP 2
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US 07/454,450
21-DEC-1989
UMBER: US 07/636,662
02-JAN-1991
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19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        61 GSQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                      61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08450246 Patent No. 5670617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-NOV-1993 ATTORNEY/AGENT INFORMATION:
TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                       83; Conservative
                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21-DEC APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-JAI
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
: New York
                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                ; STRAIN: type 1
US-08-450-257-1
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEPVDPRLEPWKHPGSQPKTACINCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FWHELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                       Score 478; DB 1;
Pred. No. 5.4e-46;
2; Mismatches 1
                                                                                                                                                                                                                                                         ORGANISM: human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION: 514

APPLICATION DATE: US 08/235,403
FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/454,450 FILING DATE: 21-BC-1989 APPLICATION NUMBER: US 07/636,662 APPLICATION NUMBER: US 07/636,662 APPLICATION NUMBER: US 08/158,015 APPLICATION NUMBER: US 08/158,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08450098 Patent No. 5674980 GENERAL INFORMATION:
INFORMATION: (212) 596-9000
TELEFAX: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 anino acid
TOPLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SUNRCE:
ORGANISM: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative
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1 MEPUDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: FAMELL, Stephen E.
APPLICANT: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 478; DB 1;
Pred. No. 5.4e-46;
2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBER: PCT/US93/07833
19-AUG-1993
MBER: US 07/454,450
                                                                  NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSOTHOVSLSKOPTSOSRGDPTGPKE 86
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; Patent No. 5804604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.6%;
nilarity 96.5%;
Conservative 2.
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TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               LENGTH: 86 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28-APR-APPLICATION NUMBER: FILING DATE: 21-AUG-APPLICATION NUMBER:
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FILING DATE: 19-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                          type 1
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
US-08-451-233-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: FAWELL, Stephen E.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEFINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/934,375
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/058,662
FILING DATE: 19-DEC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 10-DEC-1999
APPLICATION NUMBER: US 07/454,650
FILING DATE: 02-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                         Score 478; DB 1;
Pred. No. 5.4e-46;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                              ) ORGANISM: human immunodeficiency virus
) STRAIN: type 1
US-08-450-098-1
NAME: Haley Jr., James F.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 596-900
TELEFAX: (212) 596-900
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08451233
Patent No. 5747641
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                 LENGTH: 86 amander Property amino acid
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                       TOPOLOGY:
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQ 60
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Sequence 19, Application US/09030613
Sequence 19, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Florkiewicz, Robert Z.
APPLICANT: Baldd, J. Andrew
TILLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                      Length 86;
                                                                                                                                        the sequence of the TAT protein of HIV-1
                                                                                                                                                                                                                                      Score 478; DB 3; Length 86
Pred. No. 5.4e-46;
2; Mismatches 1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/NO/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 478; DB 3;
Pred. No. 5.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION.
ATTORNEY, AGENT INFORMATION:
NAME: NO. 6083706(tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                 61 GSQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                           61 GSQTHQVSLSKQPTSQSKGEPTGPKE: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.6%;
ilarity 96.5%;
Conservative
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative
                                                            MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                      ) ORIGINAL SOURCE:

INDIVIDUAL ISOLATE:

INDIVIDUAL ISOLATE:

US-07-808-452-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                            AMINO ACID
3Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POPOLOGY:
                              TYPE: AMI
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-030-613-19
                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 478; DB 1; Length 86
Pred. No. 5.4e-46;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                           human immunodeficiency virus
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERNEC/COCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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Patent No. 6063612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0860
INFORMATION FOR SEC ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.5%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fabian, Gary R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           ; STRAIN: type 1
US-08-450-236-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94306
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                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Indels

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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                      APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FWBELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
Pred. No. 5.4e-46;
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JWN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 121 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: B170 CIP 2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
                                                                                                                                                                                 61 GSQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                       61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08235403
Patent No. 6316003
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
ilarity 96.5%;
Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
Best Local Similarity
Matches 83; Conserv
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US-08-235-403-1
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Fatent No. 6306613
GENERAL INFORMATION:
APPLICANT: Andrew Baird
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
ITILE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TILLE OF INVENTION: MODULATORS OF IDENTIFYING AND USING THE SAME
FILE REFERENCE: 200124 402C4
CURRENT PAPLICATION NUMBER: US/09/451,905
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
SSO ID NO 19
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQ 60
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96.5%; Pred. No. 5.4e-46;
ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Human imunodeficiency virus type 1
US-09-124-900-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US/09/124,900
PRIOR FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
LENGTH: 86
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                                          61 GSQTHQVSLSKQPTSQSRGDPTGPKE 86
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                     61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                        Sequence 6, Application US/09124900
Patent No. 6268484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-Vaccines
                                                                                                                                                                                                                                                                                                                           APPLICANT: PURTSCHER, MARTEIN
APPLICANT: TRKOLA, Alexandra
APPLICANT: SCHMATZ, Christine
APPLICANT: SCHMATZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: KLIMA, Annelies
APPLICANT: MUSTER, Thomas
TITLE OF INVENTION: HIV-Veccin
                                                                                                                                                                                                                                                              BUCHACHER, Andrea
ERNST, Wolfgang
BALLAUN, Claudia
                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: KATINGER, Hermann
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Best Local Similarity 96.5
Matches 83; Conservative
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; ORGANISM: Homo sapien
US-09-451-905-19
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g δ

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Length 86;

DB 4;

Score 478;

86.6%;

Query Match

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Sequence 2, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
APPLICANT: Immunobiology Research, Extracellular
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08505210
Patent No. 598128
GENERAL INFORMATION:
APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: 1737 King Street, Suite 500
                                                                                                                                                                                                                                                                                                 Spring House Corporate Cntr, PO Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWAREN: APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 478; DB 5;
Pred. No. 5.4e-46;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                             Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
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LENGTH: 86 amino acids
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
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US-08-505-210-1
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STATE:
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                                                                                                                      1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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                      Length 86;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10770
                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9210770
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on TITLE OF INVENTION: RNA-Binding Proteins NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                    Score 478; DB 4;
Pred. No. 5.4e-46;
2; Mismatches 1;
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86.6%; Score 478; DB 5;
Best Local Similarity 96.5%; Pred. No. 5.4e-46;
Matches 83; Conservative 2; Mismatches 1
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19921211
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REFERENCE/DOCKET NUMBER: P-2962
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 859-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                             61 GSQTHQVSLSKQPTSQSRGDPTGPKE 86
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                                                                                                                                                                           61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: CA
                  86.6%;
llarity 96.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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INDIVIDUAL ISOLATE:
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                             Length 86;
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TITLE OF INVENTION: Natural Human 1gM Antibodies
NUMBER OF SEQUENCES: 15
NUMBER OF SEQUENCES: 15
ADDRESSDES: Darby & Darby
STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                       Score 462; DB 4;
Pred. No. 3.2e-44;
2; Mismatches 4
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLESSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, JOSEPH, R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 4436/16060US4
TELECOMMUNICATION INFORMATION:
TELECHONE: (212)527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                ORGANISM: Human immunodeficiency virus type US-09-099-333-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GSQTHQVSLSKQPTSQPRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08053079A, Patent No. 5606026; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
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                                                                                                                                                                                                                                                                    83.7%;
milarity 93.0%;
Conservative 2
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SEQ ID NO 1
LENGTH: 86
TYPE: PRT
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amino acid
enwess: single
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 80; Conserva
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: New York
RY: U.S.A.
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NUMBER OF SEQ ID NOS:
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Matches 78; Conserv
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US-08-053-079A-15
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US-08-053-079A-15
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APPLICANT: MEHTALI, Majid
APPLICANT: GUSS, Tania
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL
TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT
FILE REFERENCE: 017753-091
CURRENT APPLICATION NUMBER: US/09/099,333A
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: FR 93 14914
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER FILING DATE: 1994-03-21
EARLIER FILING DATE: 1994-03-21
EARLIER FILING DATE: 1995-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%; Score 462; DB 2; Length 86; llarity 93.0%; Pred. No. 3.2e-44; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                             COFFRAINS SISIEM:
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER:
RELING DATE:
RILNG DATE:
REPLICATION NUMBER:
CLASSIFICATION NUMBER:
REPLICATION N
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                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                         United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                   COMPUTER READABLE FORM:
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Best Local Similarity
Matches 80; Conserv
                                                                                      22314-2756
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                                                         COUNTRY:
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Length 72;

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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Goldstein, Gideon
TITLE OF INVENTION: Methods and Compositions for Impairing
TITLE OF INVENTION: Multiplication of HIV-1
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Spring House Corporate Cntr., P.O. Box 457 CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/893,853
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Pred. No. 1.1e-35;
O; Mismatches 5;
                                                                                                                Score 408; DB 4;
Pred. No. 2.4e-38;
0; Mismatches 1;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5891994
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NAME: Bak, Mary E
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GGP2
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-540-9200
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93.1%;
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98.6%;
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Best Local Similarity 93.1
Matches 67; Conservative
                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-893-853-1
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                    ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-451-905-17
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Best Local Similarity
Matches 71; Conserv
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    LENGTH: 72
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Patent No. 6306613
GENERAL INFORMATION:
APPLICANT: Robert z. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
FITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
FILE REFERENCE: 200124.402C4
                                                                                          Sequence 17, Application US/09030613
Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: Florklewicz, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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98.6%; Pred. No. 2.4e-38;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                             ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARRACTERISTICS:
LENGTH: 72 amino acids
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CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
61 ESQTHQVSLSKQPTSQSRGDPT
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Best Local Similarity 98.6
Matches 71; Conservative
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61 GSQTHQVSLSKQ 72
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STATE: Washington
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US-09-030-613-17
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STREET: 63
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                                                         RESULT 16
US-09-030-613-17
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Length 72;

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GENERAL INFORMATION:
GENERAL INFORMATION:
BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, EDITOR J.
TITLE OF INVENTION: REPRESSORS
NUMBER OF INVENTION: REPRESSORS
CORRESPONDENCE: 33
CORRESPONDENCE ADDRESS:
                                                                              CURPOTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,128A
FILING DATE: 24-SEP-1993
CLASSIFICATION: 517
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/646,998
RILING DATE: 28-JAN-1991
PRIOR APPLICATION NUMBER: PCT/US92/00652
RILING DATE: 28-JAN-1991
RIDRAPLICATION NUMBER: PCT/US92/00652
ATTORNEY/AGENT: INFORMATION:
NUMBER: ABS-JAN-1992
ATTORNEY/AGENT: INFORMATION:
NUMBER: ABS-JAN-1992
ATTORNEY/AGENT: INFORMATION:
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COMPUTER: IBM PC COMPAILLLE
OPERATUR: SYSTEM: PC-DOS/MS-DOS:
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 2.3e-32;
6; Mismatches 13
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APPLICATION NUMBER: US/08/455,674
FILING DATE: 31-MAY-1995
CTASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/SDOCKET NUMBER: B156IP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 27, Application US/08455674
; Patent No. 5616559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 312 amino acids amino acid
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Best Local Similarity 70.28
Matches 66; Conservative
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                  ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods and Compositions for Impairing TITLE OF INVENTION: Multiplication of HIV-1 NUMBER OF SEQUENCES: 124 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27. Application US/08094128A
Fatent No. 5595884
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: BARSOUM, James G.
APPLICANT: ANDROPHY, Elliot J.
TITLE OF INVENTION: REPRESSORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.6%; Score 384; DB 4; Length 72
93.1%; Pred. No. 1.1e-35;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,921
                                                                                                                                                                                                             ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O.
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,853
FILING DATE: 11-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MATY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GGP2AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFRAX: 215-540-5818
                             Sequence 1, Application US/09113921
Patent No. 6193981
GENERAL INFORMATION:
APPLICANT: Goldstein, Gideon
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.6
Best Local Similarity 93.1
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-113-921-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GSQTHQVSLSKQ 72
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                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCOVCFITAALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                  DB 1; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BARSOUM, James G.
APPLICANT: ANDROPHY, Elliot J.
TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION
TITLE OF INVENTION: PAPILLOMAVIRUS E2 TRANS-ACTIVATION
TITLE OF INVENTION: PAPILESSORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: F151 & New YORK
STREET: 1251 Avenue of the Americas
CITY: New YORK
STATE: New YORK
COUNTRY: USA
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,972
FILING DATE: 31-MAY 1995
CLASSIFICATION NUMBER: US/08/455,972
FILING PAPLICATION DATA:
APPLICATION NUMBER: US 08/094,128
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: US 07/646,998
FILING DATE: 28-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00652
FILING DATE: 28-JAN-1991
APPLICATION NUMBER: PCT/US92/O0652
FILING DATE: 28-JAN-1991
APPLICATION NUMBER: PCT/US92/O0652
FILING DATE: 28-JAN-1991
                                                                                                                                                                                                                                                                                                                                                        .3e-32;
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.3e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GSSMAGAGRIYYSR-----FGDEAARFSTIGHY 88
                                                                                                                                                                                                                                                                                                                                  Score 360.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GSQ---THQVSLSKQPTSQSKGEPTGPKETSGHH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECESTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B156CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08455972 Patent No. 5667965 GENERAL INFORMATION:
27,794
                                                             TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             Query Match 65.3%;
Best Local Similarity 70.2%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,
                                                                                                                                                                 : 312 amino acids
amino acid
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                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-455-992-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BARSOUM, James G.
APPLICANT: ANDROPHY, Elliot J.
TITLE OF INVENTION: PAPILLCMAVIRUS E2 TRANS-ACTIVATION
TITLE OF INVENTION: REPRESSORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FIGH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,992
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,128
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: US 07/646,998
FILING DATE: 28-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 360.5; DB 1;
Pred. No. 2.3e-32;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GSQ---THQVSLSKQPTSQSKGEPTGPKETSGHH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GSSMAGAGRIYYSR-----FGDEAARFSTIGHY 88
              APPLICATION NUMBER: US 08/094,128
FILING DATE: 24-SEP-1993
APPLICATION NUMBER: US 07/646,998
FILING DATE: 28-JAN 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00652
FILING DATE: 28-JAN 1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B156CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00652
FILING DATE: 28-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-455-992-27; Sequence 27, Application US/08455992; Patent No. 5656599
                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                  : 312 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.3
Best Local Similarity 70.2
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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STREET: P.O. Box 4433
CITY: Houston
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                   Texas
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US-07-910-867B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPVDPRLEPWKHPGSQPRTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                   1. MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQ 60
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                                                                                  DB 1; Length 312;
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                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BIOGEN, INC.
APPLICANT: NEW ENGLAND MEDICAL CENTER,
APPLICANT: HOSPITALS, INC.
APPLICANT: BARSOUM, James G. (US only)
APPLICANT: ANDROPHY, Elliot J. (US only)
TITLE OF INVENTION: REPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
CUUNTY: USA
ZIP: 10022-6250
COMBUTER READBLE. FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 360.5; DB 5;
Pred. No. 2.3e-32;
6; Mismatches 13;
                                                                              Query Match 65.3%; Score 360.5; DB 1; Best Local Similarity 70.2%; Pred. No. 2.3e-32; Matches 66; Conservative 6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSQ---THQVSLSKQPTSQSKGEPTGPKETSGHH 91
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                                                                                                                                                                                                                                                                     61 GSQ---THQVSLSKQPTSQSKGEPTGPKETSGHH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US92/00652
FILING DATE: 19920128
CLASSIFICATION: 435
ATTORREY/AGENT INPORMATION:
NAME: Haley Jr., James F.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 1156CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application PC/TUS9200652 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.2%;
Matches 66; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 875 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 312 amino acids
AMINO AÇID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212)715-0673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein
PCT-US92-00652-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
; MOLECULE TYPE:
US-08-455-972-27
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b; Pred. No. 4.8e-32;
1; Mismatches 11; Indels
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Patent No. 5597895
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B.
APPLICANT: Garcia, Joseph A.
APPLICANT: Harrich, David
ITILE OF INVENTION: Transdominant Tat Mutants and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 22
                                                                APPLICANT: Gaynor, Richard B.
APPLICANT: Garcia, Joseph A.
APPLICANT: Harrich, David
TITLE OF INVENTION: Transdominant Tat Mutants and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/910,867B
FILING DATE: 02-JUL-1992
CLASSIFICATION: 435
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                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee
Sequence 2, Application US/07910867B
Patent No. 5597895
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGIESTRATION UNDRER: 33,732
REFERENCE/DOCKET NUMBER: UTSD
TELEBOOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 60; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 72 amin.
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512/474-7577
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/07910867B
Patent No. 5597895
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Garor, Accept A.
APPLICANT: Garcia, Joseph A.
APPLICANT: Harrich, David
TITLE OF INVENTION: Transdominant Tat Mutants and Uses
TITLE OF INVENTION: Transdominant Tat Mutants and Uses
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: STATE RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/910,867B FILING DATE: 02-JUL-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                              Score 324; DB 1;
Pred. No. 4.7e-29;
                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                       UTSD: 263/MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                              58.7%;
77.8%;
Mayfield, Denise L
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 amino acids
                                                                                                            TELEX: N/A INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-910-867B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 72;
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Pred. No. 1e-29;
1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gaynor, Richard B.
APPLICANT: Garcia, Joseph A.
APPLICANT: Garcia, Joseph A.
APPLICANT: Harrich, David
TITLE OF INVENTION: Transdominant Tat Mutants and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/MAY
TELECOMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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02-JUL-1992
03-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                             TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 02-JUL-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.8
Best Local Similarity 79.2
Matches 57; Conservative
 P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-07-910-867B-5
                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GSQTHQVSLSKQ 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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APPLICANT: Gaynor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Texas
                                      Texas
                                             COUNTRY: US
ZIP: 77210
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US-07-910-867B-3
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                     APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: FEPINSKY, R. B.
TITLE OF INVENTOR: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
         Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
      Score 276; DB 1;
Pred. No. 7.1e-24;
0; Mismatches 1;
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FILING DATE: 25-MAY-1995
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 19-MG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-MG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 19-MG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1999
APPLICATION NUMBER: US 07/454,650
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-MOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTATION NUMBER: 27,797
REGISTATION NUMBER: 27,797
REGISTATION NUMBER: 27,797
REGISTATION NUMBER: 27,797
REGISTATION NUMBER: 27,707
REGISTATION NUMBER: 27,707
REFERENCE/DOCKET NUMBER: 27,707
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REGISTATION NUMBER: 27,707
REFERENCE/DOCKET NUMBER: 27,707
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Sequence 7, Application US/08450246
; Patent No. 5670617
                                                                                                                                                                  Query Match
Best Local Similarity 76.4%;
Matches 55; Conservative
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TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                              61 GSQTHQVSLSKQ 72
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US-08-450-246-7
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                                                                                                                           1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                            Score 310; DB 1; Length 72;
Pred. No. 1.7e-27;
1; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/450,257
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: 314

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766

FILING DATE: 28-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haley Jr., James F.
REGISTRAILON NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08450257
Patent No. 5652122
GENERAL INFORMATION:
   56.2%;
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Query Match
Best Local Similarity 75.07
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FRANKEL, Alan APPLICANT: PABO, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-JUJ APPLICATION NUMBER:
                                                                                                                                                                                                                                                   61 GSQTHQVSLSKQ 72
                                                                                                                                                                                                                                                                                       New York
: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
US-08-450-257-7
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Query Match 50.0%; Score 276; DB 1; Length 56; Best Local Similarity 76.4%; Pred. No. 7.1e-24; Matches 55; Conservative 0; Mismatches 1; Indels 16; Gaps
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Search completed: August 26, 2002, 08:10:41 Job time: 130 sec

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Mon Aug 26 09:05:59 2002
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trans-activating transcription regulator - human immunodeficiency virus type 1 (isola C; Species: human immunodeficiency virus type 1, HIV-1
A;Note host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998
C;Accession: A04017
R;Arya, S.K.; Gallo, R.C.
R;Arya, S.K.; Gallo, R.C.
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity A;Reference number: A94093; MUID:86177573
                                                                                                                                       ; Search time 50.45 Seconds
(without alignments)
180.941 Million cell updates/sec
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trans-activating t
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1 MEPVDPRLEPWKHPGSQPKT......QSKGEPTGPKETSGHHHHH 95
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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length: 2000000000
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A;Cross-references: EMBL:211530; NID:g60192; PIDN:CAA77625.1; PID:g60196
R;Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chul, S.; Min, X.; Erfle, H.; Sumner Nucleic Acids Res. 20, 5311-5320, 1992
A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activato A;Reference number: $26385; MUID:93065196
A;Accession: $26385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
trans-activating transcription regulator - human immunodeficiency virus type
          C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Oct.1994 #sequence_recy virus type 1, HIV-1
C;Accession: S33982; S26385; S19864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: EMBL:X64650; NID:g60144; PIDN:CAA45921.1; PID:g60145
C;Genetics:
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Pred. No. 2e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: AIDS trans-activating transcription regulator
Keywords: AIDS; immunodeficiency
                                                                                                       R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession S33982
A;Accession type: DNA
A;Molecule type: DNA
A;Residues: 1-86 <CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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96.58;
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A; Residues: 1-86 <SID>
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Best Local Similarity
Matches 83; Conserv
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Superfamily: A
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C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jul-1998 C; Accession: E44001  
R; Li, Y; H; H; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M. J. Virol. 66, 6587-6600, 1992  
A; Title: Complete nucleotide sequence, genome organization, and biological propertie A; Reference number: A44001; MUID:93021387
                                                                                                                                                                                                                                                           trans-activating transcription regulator - human immunodeficiency virus type 1 (stra
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R;Hoffmann, S.; Willbold, D.
Biochem. Biophys. Res. Commun. 235, 806-811, 1997
A;Title: A selection system to study protein-RNA interactions: Functional display. A;Reference number: JC5591; WUID:97350867
A;Accession: JC5591
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C,Species: human immunodeficiency virus type 1, HIV-1
C,Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                              N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 101;
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    9; Indels
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C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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Pred. No. 1.7e-30;
7; Mismatches 12
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Pred. No. 1.4e-32;
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    Mismatches
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1 Similarity 77.9%;
67; Conservative
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    Conservative
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Best Local Similarity
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Best Local Similarity
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A; Residues: 1-101 <LIY>
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KP Pang, S;: Vincers, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A:Reference number: 216673
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
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                                                                                                                                                            Score 470; DB 1; Length yo
Pred. No. 1.2e-36;
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              A Molecule type: DNA
A:Residues: 1-95 <ARY>
C:Genetics:
A:Genetics:
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS: immunodeficiency: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: AIDS trans-activating transcription regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T09446
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 6e-36;
2; Mismatches
                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                      61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                             85.1%;
95.3%;
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Best Local Similarity 93.0%;
Matches 80; Conservative
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-101 <PAN>
A; Accession: A04017
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C; Superfam'
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Length 101;

Score 429; DB 2; Pred. No. 7.6e-33;

77.78; 85.18;

Query Match Best Local Similarity

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86

GSQTHQVSLSKQPTSQSKGEPTGPKE

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    human immunodeficiency virus type 1 (isola

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                                                                                                            Galibert, F.; Hampe,
                                                                                 C. Accession: J00071
R. Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe Gene 81, 275-284, 1989
A. Title: Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human A. Reference number: J00065; MUID: 90034200
A. Reference number: J00065; MUID: 90034200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trans-activating transcription regulator - human immunodeficiency virus type 1 (
C.Species: human immunodeficiency virus type 1, HIV-1
C.bate: 30-Jun-1988 *sequence_revision 30-Jun-1988 *textichange 02-Jul-1998
C.Accession: B25523
R.Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence analysis of
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01665
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis
A;Reference number: Z14389; MUID:86245056
trans-activating transcription regulator - human immunodeficiency virus type
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-86 <SPI>
A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA44866.1; PID:g328155
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: K03456; NID: 960228; PIDN: CAA28015.1; PID: 960233
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                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 71.6%; Score 395; DB 1; I
Best Local Similarity 74.4%; Pred. No. 9.1e-30;
Matches 64; Conservative 11; Mismatches 11;
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Pred. No. 4.5e-29;
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A;Molecule type: mRNA
A;Residues: 1-87 <ALI>
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C;Superfamily: AIDS trans-activating transcription
C;Keywords: AIDS; immunodeficiency; transcription
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55; Conservative
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Best Local S
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534381
tat protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HTV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C;Accession: S54381
R;Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Accession: S5437
A;Accession: S5437
A;Accession: S5438
A;Status: preliminary
A;Moleoule Type: genomic RNA
A;Residues: 1-86 < THE>
A;Cross-references: EMBL:M22639; NID:q329377; PIDN:AAA45363.1; PID:q329378
C;Superfamily: AIDS trans-activating transcription regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          it protein · human immunodeficiency virus type 1
Species: human immunodeficiency virus type 1, HIV-1
Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
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Pred. No. 3.2e-30;
6; Mismatches 13; Indels
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Pred. No. 3.2e-30;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Introns: 72/2
Superfamily: AIDS trans-activating transcription regulator
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61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86 

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Query Match 72.5%; Best Local Similarity 77.9%; Matches 67; Conservative

RESULT

GSQTHQVSLSKQPTSQSKGEPTGPKE 86

72.5%; ilarity 76.7%; Conservative

Local Similarity

Query Match

99

Matches

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Aloute: host Homo sapiens (man)
Cloate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
Cloate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
Cloate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999
Cloate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 15.30-Jul-1999
Ribasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki
AIDS Res. Hum. Retroviruses 5, 593-644, 1989
A; Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergen
A; Reference number: J8332, MUD:90122350
A; Residues: 1-130 CHAS>
A; Residues: 1-130 CHAS>
A; Residues: 1-130 CHAS>
A; Residues: 1-130 CHAS>
A; Ross-references: GB:M30895; GB:D00477; NID:9325709; PIDN:AAA43929.1; PID:9325710
A; Note: this sequence was submitted to JIPID, October 1989
C; Genetics:
A; Introns: 99/2
C; Superfamily: AIDS trans-activating transcription regulator
C; Keywords: AIDS; transcription regulation
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C; Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C; Accession: F33943
F; Kumar, P: Hul, H:, Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.J. Virol. 64, 890-901, 1990
A; Title: Molecular characterization of an attenuated human immunodeficiency virus ty;
A; Reference number: A33943; MUID:90112662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trans-activating transcription regulator - human immunodeficiency virus type 2 (isola
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                         A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-100 <HUE>
A.Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36404.1; PID:9763084
C.Genetics:
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                     nucleic acid sequence not shown; translation
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C;Species: human immunodeficiency virus type 2, HIV-2
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Pred. No. 2.2e-09;
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A;Introns: 73/2
C;Superfamily: AIDS trans-activating transcription
C;Keywords: AIDS; immunodeficiency; transcription
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Pred. No. 2.2e-
2; Mismatches
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60.7%; Pred
tive 12; I
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nes 35; Conserv
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Best Local Si
Matches 54)
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Matches
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R. Michael, N. L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir J. Virol. 69, 4228-4236, 1995
A. Virol. 69, 4228-4236, 1995
A. Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lon A; Reference number: 216654; MUID:95287475
A; Accession: T09384
A; Accession: T09384
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
B; Residues: 1-71 < MIC>
A; References: EMBL:U24451; NID:9829440; PIDN:AAA79576.1; PID:9829444
C; Genetics:
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Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human A;Reference number: A94136; MUID:87041461
A;Accession: B25523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - human immunodeficiency virus type 1 (isolate
                                                                                                                                          Amolecule type: DNA
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES>
A/Residues: 1-72 <DES
C/Residues: 1-7
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 364; DB 1; Le
Pred. No. 5.7e-27;
0; Mismatches 8;
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Pred. No. 5.9e-26;
4; Mismatches 8;
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Local Similarity 88.9%;
Les 64; Conservative 0
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Best Local Similarity 83.1%;
Matches 59; Conservative
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Best Local Si
Matches 64
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C; Superfamil
C; Keywords:
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1990
C;Genetics:
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C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jun-2000
C; Accession: 138475; JQ0981
R; Ttistem, M.; Hill, F.; Karpas, A.
J; Gen. Virol. 72, 721-724, 1991
A; Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficier A; Reference number: A38475; MUID:91170959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 QPLEECDNSCYCKRCCYHCQLCFLKKGLGICYDRKGR-•RRRIPKKAKAHSSSASDKSIS 105
                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-133 <TRI>
A;Cross-references: GB:D00835; NID:g3153166; PIDN:BAA00714.1; PID:g221467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 QPKTACTN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQGSQTHQVSLS---- 70
                                                                                                                                                                   13;
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                                                                                                                         Length 130;
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                                                                                                                                                                   Indels
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                       A;Introns: 99/3
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.introns: 102/2
C.Superfamily: AIDS trans-activating transcription regulator
C.Keywords: transcription
                                                                                                                         ; Score 163.5; DB 1;
; Pred. No. 2.8e-08;
10; Mismatches 24;
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C;Species: human immunodeficiency virus type 2, HIV-2
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Pred. No. 4.4e-08;
3; Mismatches 20;
                                                                                                                                                                                                                                                                                                                  103 TRTGDSQPTKKQKKTVEATVET 124
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Matches 32; Conserv
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                                                                                                                                          Best_Local Similarity
Matches 35; Conserv
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553096
tat protein - human immunodeficiency virus type 2
C; Species: human immunodeficiency virus type 2
C; Species: human immunodeficiency virus type 2, HIV-2
C; Species: human immunodeficiency virus type 2, HIV-2
C; Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C; Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C; Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C; Date: 08-Jul-1995 #sequence_revision 23-Jul-1995 #text_change 20-Sep-1999
R; Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
R; Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
A; Reference number: S53091
A; Reference number: S53091
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-130 < REC>
A; Coss-references: EMBL: 248731; NID: 9732718; PIDN: CAAB8625.1; PID: 9732724
C; Genetics:
A; Introns: 99/2
C; Superfamily: AIDS trans-activating transcription regulator
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A;Accession: F33943
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Cossides: 1-130 cKUN>
A;Crossides: 1-130 cKUN>
C;Genetics: A;Gene: tat
A;Gene: tat
C;Genetics: 99/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription
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Pred. No. 6.4e-09;
8; Mismatches 26;
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46.5%; Pred. No. 6.4e-09;
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Best Local Similarity 47.9%;
Matches 34; Conservative
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R;Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kita. Nature 33, 457-461, 1988
Nature: Sequence of simian immunodeficiency virus from African green monkey, a new A;Reference number: A30045; MUID:88232906
                                                                                                                                                                                                                                                                                                                                                                    Cispecies: human immunodeficiency virus type 2 D205 Cispecies: human immunodeficiency virus type 2 D205 Cispecies: human immunodeficiency virus type 2 D205, HIV-2 D205 Cispecies: human immunodeficiency virus type 2 D205, HIV-2 D205 Cispecies: human immunodeficiency virus type 2 D205, HIV-2 D205 Cispecies: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Jul-1998 Cispecies: 080840 Cispecies: N: Seipp, A:; Kuehnel, H:; Ruebsamen-Walgmann, Mitule: A highly divergent HIV-2 related isolate.

A:Reference number: S08434; MUID:90081881
A:Reference number: s08440
A:Reterence number: sound sequence not shown; translation not shown
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A; Cross-references: EMBL:X07005; NID:g61748; PIDN:CAA30661.1; PID:g4469309
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                                                                                                                                 1 MEPVDPRLEPWKHPGSQ---PKTACTN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRR 56
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          Length 106;
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C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 73/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS: immunodeficiency; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
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A;Note: this sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 142; DB 1;
Pred. No. 2.2e-06;
9; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 OPKTACTN-CYCKKCCFHCOVCFITAALGISYGRKKRRORRR
       ; Score 149; DB 1;
; Pred. No. 5.3e-07;
13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
          27.0%;
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Local Similarity 57.1%;
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 39.5%;
Matches 30; Conservative
                                                      Conservative
                                                                                                                                                                                                                                   | |:::: | |
59 RIPKKAKANTSSAS 72
                                                                                                                                                                                                      57 RPPQGSQTHQVSLS 70
                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-96 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                        32;
       Query Match
Best Local S:
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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C.Species: simian immunodeficiency virus, SIV
C.Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 02-Jul-1988
C.Accession: F28887
R.Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P. Artle: Sequence of simian immunodeficiency virus from macaque and its relationship to A.Reference number: A28887; MUD:87287230
A.Reference number: A28887; MUD:87287230
A.Residues: 1-129 <CHA>
A.Residues: 1-129 <CHA>
A.Residues: 1-129 <CHA>
A.Gross-references: GB:Y00277; GB:M16403; NID:g61730
C.Genetics:
A.Gene: tat
A.Introns: 98/3
C.Superfamily: AIDS trans-activating transcription
C.Superfamily: AIDS: immunodeficiency; transcription
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Cell 49, 307-319, 1987
A.Title: The genome organization of STLV-3 is similar to that of the AIDS virus except
A.Reference number: A26737; MUID:87187627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trans-activating transcription regulator - simian immunodeficiency virus SIVagm (type C.Species: simian immunodeficiency virus SIVagm C.Date: 31-Mar-1989 *sequence_revision 31-Mar-1989 *text_change 02-Jul-1998
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                                                                                                                                                                                                    --OPKTACIN-CYCKKCCFHCOV 36
                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                 37 CFITAALGISYGRKKRRQRRRPPQGSOTHQVSLS-----KQPTSQSKGEP
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                                                                                                    Length 130;
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C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; transcription
       transcription regulator
                                                                                                  Query Match 29.2%; Score 161; DB 2; Le
Best Local Similarity 33.9%; Pred. No. 4.8e-08;
Matches 39; Conservative 12; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.4%; Score 151; DB 1; L. Best Local Similarity 43.1%; Pred. No. 4e-07; Matches 31; Conservative 9; Mismatches 20;
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A;Note: the authors translated the codon GAC
C;Genetics:
A;Gene: tat
C; Superfamily: AIDS trans-activating C; Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 RIRLCOPKKAKK 114
                                                                                                                                                                                                 2 EPVDPRLEPWKHPGS-
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A; Residues: 1-106 <HIR>
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trans-activating transcription regulator - bovine immunodeficiency virus (isolate 127 C; Species: bovine immunodeficiency virus C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Jul-1998 C; Accession: D34742
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C;Species: simian immunodeficiency virus, SIV
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 02-Jul-1998
                                                                                                                                                                                                                          Rilirsch, V.M.; Martin, J.E.; Dapolito, G.; Elkins, W.R.; London, W.T.; Goldstein, S. J. Virol. 68, 2649-2661, 1994
Affilte: Spontaneous substitutions in the vicinity of the V3 analog affect cell tropi A; Accession: T11557
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A;Title: Genetic characterization of simian immunodeficiency virus isolated from an A;Reference number: A48344, MUID:92352315
A;Recession: A48344
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C;Accession: T11557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
*Molecule type: DNA
A;Residues: 1-131 <HIR>
A;Cross-references: EMBL:U04985; NID:g451609; PID:g451613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 24.2%; Score 133.5; DB 2; Best Local Similarity 38.4%; Pred. No. 1.7e-05; Matches 28; Conservative 12; Mismatches 18;
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Pred. No. 0.00014;
8; Mismatches 17;
                                                                                tat protein – simian immunodeficiency virus SIVsm
                                                                                                           C;Species: simian immunodeficiency virus SIVsm A;Variety: strain 62
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llarity 44.2%;
Conservative E
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A; Residues: 1-116 <SAK>
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Best Local Simi
Matches 23;
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C;Species: simian immunodeficiency virus SIVsm
A;Variety: strain E543
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T11564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 PLKRCTNKCYCKCCCYHCQLCFLQKGLGVTYHAPRIRRKKIAPLDRFPEQKQSISTRGRD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1119 <BAI>
A;Cross-references: GB:M30931; NID:9334400; PIDN:AAA91917.1; PID:9334401
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A;Introns: 73/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 139.5; DB 2;
; Pred. No. 4.3e-06;
14; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 PKTACTN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 138.5; DB 2 36.6%; Pred. No. 5.8e-06; tive 14; Mismatches 26
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Best Local Similarity 30.6%
Matches 30; Conservative
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Best Local Similarity 36.6%
Matches 26; Conservative
104 STRTRNROPKK 114
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Gaps

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Length 1001; Indels --ннннн 897

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A; Cross-references: EMBL:U42841; PIDN:AAC48171.1; GSPDB:GN00021; CESP:T17H7.5 A; Experimental source: strain Bristol N2; clone T17H7 C; Genetics: C; Genetics: A; Gene: CESP:T17H7.5 A; Map position: 3 A; I40/3; 762/3; 795/3; 840/3; 942/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ALGISYGRKKRRQRRRPPQGSQ-THQVSLSKQPTSQSKGEPTGPKETSGHHHHHH 95
                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
1.3;
                                                                                                                                                                                                                                                                                                                                                                                         Score 88; DB 2
Pred. No. 1.3;
5; Mismatches
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Best Local Similarity 38.2%;
Matches 21; Conservative
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Accession: S46349
;Jin, M.J.; Hul, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.;
MBO J. 13, 2935-2947, 1994
MBO J. 13, 2935-2947, 1994
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R;Garvey, K.J.; Oberste, M.S.; Elser, J.E.; Braun, M.J.; Gonda, M.A.
Virology 175, 391-409, 1990
A;Ittle: Vucleotide sequence and genome organization of biologically active proviruses
A;Reference number: A34742; MUID:90223985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Crossreferences: EMBL:U04005; NID:g466229; PIDN:AAA21507.1; PID:g466233 A;Experimental source: isolate SAB-1; sabaeus monkey A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993 A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: T28897
C:Accession: T28897
R:Favello, A.
Submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid T17H7.
A:Reference number: 220540
A:Accession: T28897
A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 PKTACTNCYCKKCCFHCQVCFITAALGISYGR-----KKRRQRRRPPQGSQTHQVS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence not shown; translation not shown Molecule type: DNA Residues: 1-73 <JIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                         A Molecule type: genomic RNA
A Residues: 1-145 <GAR>
A Cross-references: GB:M32690
C Genetics:
A Gene: tat
A:Introns: 103/3
C Superfamily: AIDS trans-activating transcription regulator
C; Reywords: AIDS; immunodeficiency; transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112; DB 2; Le
Pred. No. 0.001;
6; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 114.5; DB 1;
; Pred. No. 0.001;
10; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternate names: tat protein
Species: simian immunodeficiency virus SIVagm
Variety: isolate SAB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%;
32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.3%;
Best Local Similarity 46.3%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 32.99
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQRSFTNMDQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 LSKQPTSQSK 78
                                                                                                                                                     A; Accession: D34742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
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OM protein - protein search, using sw model

August 26, 2002, 08:15:43; Search time 40.39 Seconds (without alignments) 91.071 Million cell updates/sec Run on:

US-09-509-239-23 552 1 MEPVDPRLEPWKHPGSQPKT ......QSKGEPTGPKETSGHHHHH 95 ritle:
Perfect score:
Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 105224 segs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	!		1mmun	1mmun	1mmun	immun	immun	immun	1mmun	immun	1mmun	1mmun	immun	1mmun	1mmun	1mmun	1mmun	1mmun	1mmun	1mmur	1mmun	1mmn	immun	nzee	1mmun	1mmun	immun	immun	1mmun		immu	immun	1mmun	immun
	ption	huma	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	human	chimpanzee		human	human	human	human	human	simian	human	human	human
	Description		P04607	P04326	P04610	P05908	P04608	P20879	P19553	P05906	P05907	P35965	P05905	P19552	P04614	P20893	P12506	P04609	P18804	P04613	P04611	P24738	P04612	P17285	P18044	974124	P20880	P04605	P24109	P17759	P05911	809	059	P12453
SUMMARIES		181	ιPV	112	HV1BR	LRH	LH2	HV1JR	LS1	HV1SC	HV1C4	1.Y.2	IMN	183	1A2	10Y	122	971	ONI	IMA	Ξī	104	LB5	7CZ	2G1	2KR	ST	280	HV2CA	HV2D1	SIVM1	HV2BE	HV2NZ	HV2SB
SUMDS	ID		TAT_HV1PV	TAT_HV112	TAT HV	TAT_HV1RH	TAT_HV1H2	TAT_HV]	TAT_HV1S1	TAT_HV]	TAT_HV]	TAT_HV1Y2	TAT_HV1MN	TAT_HV1S3	TAT_HV1A2	TAT_HV10Y	TAT_HV1Z2	TAT_HV126	TAT_HV1ND	TAT_HV1MA	TAT_HV1EL	TAT_HV1U4	TAT_HV1B5	TAT_SIVCZ	TAT_HV2G1	TAT_HV2KR	TAT_HV2ST	TAT_HV2RO	TAT_HV	TAT_HV	TAT_SI	TAT_HV		TAT_HV
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	Length		86	86	96	102	98	101	101	101	101	101	101	101	101	101	98	98	98	87	66	101	28	100	130	130	130	130	133	130	130	130	130	130
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	Score	478	473	470	462	453	446	438	430	429	427	426	423	423	411	411	400	400	m	387.5	384	342	S.	315.5	ഗ	_	20	163.5	61	~	20	158.5	∞ •	153.5
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	P15835										
	-	-				٠	-	-			
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100	σ	٥١	H	H	Ä	H	Ξ	11	11	11	4
	26.9			•		•					
27.0		26.7	26.5	25.9	25.7	25.3	24.7	24.5	23.1	22.1	21.0

## ALIGNMENTS

RESULT	ULT 1
TAT	
Q C	TAT_HVIBI STANDARD; PRI; 80 AA. PO4606:
2 5	1987 (Rel.
ā	(Rel. 05,
Ę	_
Œ	TAT protein (Transactivating regulatory protein).
GN	
SO	type 1 (BH10 isolate) (
SO .	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
႘	Viruses; Retroid viruses; Retroviridae; Lentivirus.
ŏ	NCBI_TaxID=11678, 11707;
RN	(1)
RP P	SEQUENCE FROM N.A.
<u>۾</u>	STRAIN-ISOLATE BH10;
XX	.2578615;
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA	Doran E.R., Rafalski J.A.,
RA	
RA	Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
RA	
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL	Nature 313:277-284(1985).
Z.	[2]
ЯP	SEQUENCE FROM N.A.
ಜ	STRAIN-ISOLATE HXB3;
КX	4ed-2988795;
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
RA	F., Reddy E.P.;
RT	"HTLV-III env gene products synthesized in E. coll are recognized by
RT	antibodies present in the sera of AIDS patients.";
RL	Cell 41:979-986(1985).
႘	-! FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
ខ	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
႘	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
႘	PROMOTER. •
႘	-!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
႘	-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
ပ္ပ	-!- MISCELLANEOUS: THE TWO ISOLATES TAT SEQUENCE ARE IDENTICAL.
႘	
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႘	between the Swiss Institute of Bioinformatics and the EMBL outstation
ပ္ပ	the European Bioinformatics Institute. There are no restrictions on its
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DR	EMBL; M14100; AAA44676.1;

222222

EMBL; M15654; AAA440'0.1; -.
EMBL; M15654; AAA44199.1; -.
HIV; M15654; TAT\$BH102.
HIV; M14100; TAT\$RKB3.
InterPro; IPR001831; HIV\_TAt.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.

GSQTHQVSLSKQPTSQPRGDPTGPKE 86

61

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Nature 313:450-458(1985),
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ranscription regulation; Activator; RNA-binding; Nuclear protein;
Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
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Pred. No. 4.9e-39;
...amatches 2; Indels
                                                                              Score 478; DB 1; Length 86
Pred. No. 1.6e-39;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-85111157; PubMed-2982104;
Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V.,
Capon D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 AA; 9794 MW; 4DD5C6415FAF9015 CRC64;
                               4DD609415FAF9015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid structure and expression of the human NIDS/lymphadenopathy retrovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID=11700;
                                                                                                                                                                                                                                                                                                                                                                                                                           TAT protein (Transactivating regulatory protein).
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(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                           86 AA.
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>fam; PF00539; Tat; 1.
                                                                               86.6%;
96.5%;
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95.3%;
                               9784 MW;
                                                                              Query Match
Best Local Similarity 96.5
Matches 83; Conservative
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                               AA;
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16-OCT-2001
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P04607;
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              AIDS.
SEQUENCE
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Matches
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TAT_HV1PV
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                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=86177573; PubMed=3008154;

Arya S.K., Gallo R.C.;

Arya S.K., Gallo R.C.;

"Three novel genes of human T-lymphotropic virus type III: immune reactivity of their products with sera from acquired immune deficiency syndrome patients.";

Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).

-I-FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVARING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
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                                                                                                                            nunodeficiency virus type 1 (clone 12) (HIV-1). Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4DD609414FBE9115 CRC64;
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                                                                                              TAT protein (Transactivating regulatory protein).
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Pred. No. 9.5e-39;
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Last annotation update)
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                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   -! - SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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                86 AA
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                PRT;
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(Rel. 05, Last sequ
                                                Created)
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PIR; A04017; TNLJ12.
HIV; M11840; TAT$PCV12.
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95.3%;
                                                                                                                            Human immunodeficiency virus
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                STANDARD;
                                              (Rel. 04, (Rel. 05, (Rel. 40,
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Best Local Similarity
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                                                                                                                                                          NCBI_TaxID=11679;
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13-AUG-1987
16-OCT-2001
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13-AUG-1987
16-OCT-2001
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P04610;
              TAT_HV112
P04326;
                                                                                                                                              Viruses;
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TAT_HV1BR
1D TAT_HV
DT 13-AUG
DT 13-AUG
DT 16-OC
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GN TAT P1
OS HUMAN
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TAT_HV112
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Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).

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AIDS.
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                                                                                                         Buckler C.E., Buckler-White A.J., Willey R.L., MCCOy J.;
Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Transcription regulation; Activator; RNA-binding; Nuclear protein;
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T -> M (IN CLONE PNL4-3).

PPQG -> AHON (IN CLONE PNL4-3).

V -> A (IN CLONE PNL4-3).

P -> S (IN CLONE PNL4-3).

9B1B4A915FAF8A14 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86218077; PubMed-2423250;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
                                                    Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.; "Nucleotide sequence of the AIDS virus, LAV."; Cell 40:9-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
Retroid viruses; Retroviridae; Lentivirus
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Pred, No. 5.5e-38;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                          SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY)
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                                          PubMed-2981635;
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(Rel. 09, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                             EMBL; KO2013; AABS9745.1; -. EMBL; M19921; AAA44985.1; -. HIV; KO2013; TATSBNU. HIV; M19921; TATSNU. InterPro; IPR001831; HIV_Tat.
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PRINTS; PR00055; HIVTATDOMAIN.
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93.0%;
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Best Local Similarity 93.0
Matches 80; Conservative
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                              SEQUENCE FROM N.A.
                                            MEDLINE-85099333;
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16-OCT-2001
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P05908;
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SEQUENCE
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VARIANT
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TAT_HV1RH
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                                                                                                                                                       Cell 45:637-648(1986).
-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER.
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                           Wong-Staal F.; "Identification of conserved and variable "Identification and characterization of conserved and variable "Identification and characterization of conserved and variable "Identification".
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                                                                                             regions in the envelope gene of HTLV-III/LAV, the retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 102;
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 453; DB 1; Length 10
Pred. No. 4.7e-37;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 102 AA; 11538 MW; 3EACFB843C5195BD CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87299196; Pubmed-3040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H.,
Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 05, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                         SUBUNIT: BINDS CYCLIN TI (BY SIMILARITY)
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDS Res. Hum. Retroviruses 3:57-69(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GSQTHQVSLSKQPTSQSKGEPTGPKET 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001831; HIV_Tat. Pfam; PF00539; Tat; 1 PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M17451; AAA45050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%;
ilarity 88.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAT_HV1H2
P04608; O09778;
13-AUG-1987 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M17451;
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16-OCT-2001
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11508 MW; 3E6CBD8FF7F8D4FA CRC64;

101 AA;

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SEQUENCE
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                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                      the collaboration EMBL outstation -
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                                  This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koyanagi S., Chen I.S.Y.;
Submitted (DEC-1988) to the HIV data bank.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                       1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRAHQ 60
                                                                                                                                                                                                                                                                                                                                        1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   franscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                     Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11688;
                                                                                                                                                                                                                                                                                       Length 86;
                                                                                                                                                                                                                                                                                     Score 446; DB 1; Length 86
Pred. No. 1.9e-36;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                               4DDC56D979769115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - I - SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
         SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                            61 GSQTHQVSLSKQPTSQSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                   61 NSOTHOASLSKOPTSOPRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 17, Created)
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                                                                                                                                                                                                         PRINTS; PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
                                                                                                                                                                                 IPR001831; HIV_Tat.
BINDS CYCLIN T1
                                                                                                                                          EMBL; K03455; AAB50256.1; -.
                                                                                                                                                                                                                                                                                    80.8%;
ilarity 90.7%;
Conservative
                                                                                                                                                       AF033819; AAC82591.1;
                                                                                                                                                                                                                                               9837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; M38429; TAT$JRCSF
                                                                                                                                                                    TAT$HXB2
                                                                                                                                                                                            Pfam; PF00539; Tat; 1
                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                               86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                    HIV; K03455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991
                                                                                                                                                                                 nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAT_HV1JR
P20879;
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS.
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"Viral determinants of human immunodefictency virus type I T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";

J. Virol. 64:4390-4398(1990).

-: FUNCTION: TRANSCRIPTIONAL REGULAROR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                             Gaps
                                                                                                                        1 MEPVDPRLEPWKHPGSQPRTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                 1 MEPUDPSLEPWKHPGSQPKTACTNCYCKKCCLHCQVCFTTKGLGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   franscription regulation; Activator; RNA-binding; Nuclear protein;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 101;
                              Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 430; DB 1;
Pred. No. 7.4e-35;
                           Score 438; DB 1;
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                       101 AA.
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                                                                        Mismatches
                                                                                                                                                                                                                                             61 GSQTHQVSLSKQPTSQSKGEPTGPKET 87
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90347835; Pubmed-2384920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M65024; AAA45069.1; -.
HIV; M38428; TATSSF162.
InterPro; IPR001831; HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.9%;
85.1%;
                         79.3%;
86.2%;
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                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00539; Tat; 1.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991
01-FEB-1991
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P19553;
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MEDLINE-87041461; PubMed-3490666
                                                                                                                                                                                                                                                                                                                                                                                                  11594 MW;
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PRINTS; PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                   HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                         77.48;
86.08;
                                                                                                                                                                                                                                                                                         EMBL; M13137; AAA44309.1; -.
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Best Local Similarity 86.09
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                       PIR; B25523; TNLJH4.
HIV; M13137; TAT$CDC45.
InterPro; IPR001831; HIV
                                                                                                                                                                                                                                                                                                                                                                                                  101 AA;
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                                                                                                                                PROMOTER.
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P35965;
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                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: BINDS CYCLIN TI (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.7%; Score 429; DB 1; Length 101; 83.9%; Pred. No. 9.2e-35; ive 6; Mismatches 8; Indels
                                                                                                                   Human immunodeficiency virus type 1 (SC isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA; 11426 MW; C91090B938D15788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAT protein (Transactivating regulatory protein).
TAT.
                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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Last annotation update)
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                          101 AA.
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                                                                                                                                                                                                                                                                                                                                               1984 IN SOUTHERN CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; TAT$SC.
IPR001831; HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M17450; AAA45060.1; -.
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                           STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID-11702;
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P05907;
01-NOV-1988 (
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16-OCT-2001
                        TAT_HV1SC
P05906;
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TAT_HV1C4
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             TAT_HV1SC
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properties of human immunodeficiency virus type I in vivo: evidence for limited defectiveness and complementation.";
J. virol. 66:6587-6600(1992).
-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shaw G.M.;
"Complete nucleotide sequence, genome organization, and biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 427; DB 1; Length 101;
Pred. No. 1.4e-34;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        817D915F3FB1C7FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1 (YU-2 isolate)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=36377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein (Transactivating regulatory protein).
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                      -:- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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MEDLINE-93021387; PubMed-1404605;
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Transcription regulation; Activator; RNA-binding; Nuclear protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E., Franchini G., Reitz M.S. Jr.;
"Envelope sequences of two new United States HIV-1 isolates.";
Virology 164:531-536(1988).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
                                                                                                                                                                                                                                                                    Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
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                                                                                                                                                                                                                                                                                                                                                                77.2%; Score 426; DB 1; Length 101; 83.9%; Pred. No. 1.8e-34; 1ve 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
Viruses: Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                          101 AA; 11594 MW; 15F0F3702EFC807D CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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                                                                                                                                                                                                FIK; E44UU1; E44UU1.
InterPro; IPRO01831; HV_Tat.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
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InterPro: IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1
PRINTS; PR00055; HIVTATDOMAIN.
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P05905;
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Matches
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York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
York-Higgins and cytopathicity are linked to the envelope region of the viral genome...
J. Virol. 64:4016-4020(1990)
J. Virol. 64:4016-4020(1990)
J. Virol. 64:4016-4020(1990)
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J. Virol. 64:4016-4020(1990)
J. Virol. 64:4
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                                                                                                                                            Length 101;
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                                                     11634 MW; 2DBC7A21486389FF CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (SF33 isolate)
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                         Score 423; DB 1; I
Pred. No. 3.5e-34;
4; Mismatches 10;
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-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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Pfam; PF00539; Tat; 1.
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Best Local Similarity 83.9%;
Matches 73; Conservative
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Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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P19552;
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                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-i- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-i- MISCELLANDOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALPHY GABONESE INDIVIDUAL.
-i- MISCELLANEOUS: THE SINGLE C -> S SUBSTITUTION AT RESIDUE 22 OF THE
OXI TAT PROTEIN RENDERS IT INACTIVE, BUT MAY NOT ACCOUNT FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theodore T., Buckler-White A.;
Submitted (NOV-1988) to the HIV data bank.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                         -i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11683;
                                                                Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson & "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA; 11561 MW; 83ACAC36CC4C87AD CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 411; DB 1; L
Pred. No. 4.9e-33;
5; Mismatches 11;
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81.6%;
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Best Local Similarity 81...
Best Local 71; Conservative
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                                           SEQUENCE FROM N.A.
NCBI_TaxID=11699;
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P12506;
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DT 16-0C

DE TAT 00-0C

DE TAT 00-0C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.5%; Score 411; DB 1; Length 101; 80.5%; Pred. No. 4.9e-33; ive 4; Mismatches 13; Indels
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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Last annotation update)
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  61 SSQNHQDSLSKQPSSQPRGDPTGPKES 87
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(Rel. 40, Last ann
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Science 227:484-492(1985).
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Matches 70; Conserv
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01-FEB-1991
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16-OCT-2001
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P20893;
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P04614;
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Query Match

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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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TAT_HV1ND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Srinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
Sanchez-Pescador R.;
                                                                                                                                                                                                                                                                  72.5%; Score 400; DB 1; Length 86; 76.7%; Pred. No. 4.8e-32;
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                                                                                                                                                                                                                         86 AA; 9737 MW; 97561D72AFCFFF19 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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                                                                                                                                                                                                                                                                                              8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-87248097; PubMed-3036660;
                                                                                                                                                    InterPro; IPR001831; HIV_Tat. Pfam; PF00539; Tat; 1. PRINTS; PR00055; HIVTATDOMAIN.
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HIV; K03458; TAT$26.
InterPro; IPR001831; HIV_Tat.
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nes 66; Conserv
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P04609;
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Matches
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-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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SUBCELULALAR LOCATION: NUCLEAR; NUCLEOLAR.
MISCELLANBOUS: NDK, ISOLATEP FROM A ZAIRIAN PATIENT AFFECTED WITH
ALDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C.;
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                                                                                                                                                                                                                                                                                                                                                        the
                                                            Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of human immunodeficiency virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                     Score 400; DB 1; Length 86;
Pred. No. 4.8e-32;
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7DB9E64E0AF8B0F4 CRC64;
                                                                                                                   9736 MW; ElEOAD741FCFF5AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OZT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGOTHODPIPKOPSSOPRGNPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90034200; Pubmed=2806917;
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSQTHQVSLSKQPTSQSKGEPTGPKE
                                                                                                                                                                                                                                                                  ;
9
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001831; HIV_Tat.
                                                                                                                                                                                                        72.5%;
77.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M27323; AAA44866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9711 MW;
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; JQ0071; TNLJND.
HIV; M27323; TAT$NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001831;
Pfam; PF00539; Tat;
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                   86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAT_HV1ND
P18804;
                                                                                                                   SEQUENCE
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.
                                                                                                                                                                                                                                                                                                                                                                                                                    PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.6%;
72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11081 MW;
                                                                                                                                                                                                                                                                                                                                                             EMBL; K03454; AAA44322.1; -. HIV: K03454; TATSELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                        NCBI_TaxID-11689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-11703;
                                                                                                                                                                                                PROMOTER.
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01-MAR-1992 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                           HIV; K03454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAT protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sim
Matches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAT_HV1U4
P24738;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                           Cell 46:63-74(1986).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPO 60
              9
                                                                                                                                                                                                                                                                                                                                    nucleotide sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pranscription regulation; Activator; RNA-binding; Nuclear protein;
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 87;
                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 AA; 10036 MW; 3832412849D5B1CE CRC64;
                                                                                                                                                                                                                                                                                                                      Sonigo P.;
                                                                                                                                                                             NUG-1987 (Rel. 05, Last sequence update)

CT-2001 (Rel. 40, Last annotation update)

protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 40, Last annotation update)
(Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 387.5; DB 1
Pred. No. 7.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                      87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                  Alizon M., Wain-Hobson S., Montagnier L., "Genetic variability of the AIDS virus: nu of two isolates from African patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GSQTHQVSLSKQPTSQSKGE-PTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86245056; Pubmed-2424612;
                                         GSQTHQVSLSKQPTSQSKGEPTGPKE
                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001831; HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 70.2%;
Local Similarity 74.7%;
nes 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X04415; CAA28015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00539; Tat; 1.
                                                                                                                                                                 05,
05,
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID=11697;
                                                                                                                                                                13-AUG-1987 (
13-AUG-1987 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K03456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAT protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAT_HV1EL P04611;
                                                                                                                                      TAT_HV1MA P04613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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RESULT 20 TAT\_HV1EL

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Matches

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the European Bioinformatics Institute. There are no restrictions on its
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AIDS Res. Hum. Retroviruses 6:1073-1078(1990).
- I- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVES SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-86245056; PubMed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
Cell 46:63-74(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (strain Ugandan / isolate U455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Oram J.D., Downing R.G., Roff M., Clegg J.C.S., Serwadda D.,
Carswell J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 99;
Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B0ECD5199874A762 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 384; DB 1;
Pred. No. 1.8e-30;
); Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AA.
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Viruses; Retroid NCBI_TaxID=11723;
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                                                                                                                                                                                                                                                                                         01-AUG-1990 (
01-AUG-1990 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                    TAT protein
                                                                                                             Query Match
Best Local Simi
Matches 55;
                                                                                                                                                                                                                                                                TAT_SIVCZ
P17285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS.
SEQUENCE
                                                      NON_TER
SEQUENCE
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                                                                                                                                                                                                                                       RESULT 23
                                                                                                                                                                                                                                                  TAT_SIVCZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284(1965).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                               1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85111123; PubMed-2578615;
Sather L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
                                                                                                                                                                                                                       Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein) (Fragment)
                                                                                                                                                                                                                                                                                         62.0%; Score 342; DB 1; Length 101; 65.5%; Pred. No. 2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                                                                                                                                                                 101 AA; 11378 MW; 3C782A8055DAB249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                         SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
           BINDS CYCLIN T1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 AA.
                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             61 GSKDHQTLIPKQPLPQSQRVSAGQEES 87
                                                                                                                                                                                                                                                                                                                                                                                                    61 GSQTHQVSLSKQPTSQSKGEPTGPKET 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                         Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
                                                                                                                                                                            IPR001831; HIV_Tat.
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                                                                                                                                                                EMBL; M62320; AAA75021.1; -.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 65.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV; K02012; TAT$BH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wong-Staal F.
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13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAT_HV1B5
P04612;
                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                             nterPro;
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TAT_HV1B5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90259077; PubMed=2188136;
Huet I., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
"Genetic organization of a chimpanzee lentivirus related to HIV-1.";
Nature 345:356-359(1990).
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InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                   57
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                                                                                                                                                                                                                                                                                                                                                            1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                          Length 58;
                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 AA; 11209 MW; 1B78830B90EED50E CRC64;
                                                                                                                                        E36C21F8FFD813E3 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
(Transactivating regulatory protein).
                                                                                                                                                                                                                       Score 324; DB 1;
Pred. No. 6.3e-25;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                       58.7%;
96.5%;
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                                                                                                              58
6800 MW;
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Best Local Similarity 60.7%
Matches 54; Conservative
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                           58
58 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90122350; PubMed-2611042; MEDLINE-90122350; PubMed-2611042; MEDLINE-90122350; PubMed-2611042; MEDLINE-90122350; PubMed-2611042; Makin A.; Miki K., Hayami M.; Rukasawa M., Miki K., Hayami M.; "Genomic divergence of HIV-2 from Ghana."; AIDS Res. Hum. Retrovituses 5:593-604(1989).

-I- FUNCTION: TRANSCRIPTIONAL PREGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Activator; RNA-binding; Nuclear protein;
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(
                                                                                                                                                                                                                                                Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 175.5; DB 1; Length 49.3%; Pred. No. 2.2e-10; ive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: BINDS CYCLIN TI (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                       130 AA.
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Best Local Similarity 49.3
Matches 35; Conservative
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                                                                       STANDARD;
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HIV; M30895; TAT$2GH1.
                                                                                                                      (Rel. 16,
(Rel. 16,
(Rel. 40,
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NCBI_TaxID=73484;
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Q74124;
01-NOV-1997 (
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                                                                                                                                                  01-NOV-1990
16-OCT-2001
                                                                  TAT_HV2G1
P18044;
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SEQUENCE
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ID TAT_H

ID TAT_H

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DT 16-OC

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TAT_HV2G1
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J. Virol. 64:890-901(1990).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
Kraus G.K., Talbott R., Leavitt M., Luznick L., Schmidt A., Badel P., Bartz C., Morton W., Wong-Staal F., Łooney D.J.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Kumar P., Hul H., Kappes J.C., Haggarty B.S., Hoxie J.A., Arya S.K.,
Shaw G.M., Hahn B.H.;
"Molecular characterization of an attenuated human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 OPKTACTN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ranscription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14440 MW; 2E328084003CC6E0 CRC64;
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NCBI_TaxID=11721;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
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103 TRTGNSQTEKKQT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 QSKG-EPTGPKET 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 36; Conserv
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                                                                                                                                                          PROMOTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROMOTER.
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P20880:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
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Transcription regulation; Activator; RNA-binding; Nuclear protein;
                          HIVTATDOMAIN
 IPR001831; HIV_Tat.
               Pfam; PF00539; Tat; 1
PRINTS; PR00055; HIVT
                                                                 50
130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    TAT_HV2CA
P24109;
                                                                 MUTAGEN
                                                                                                                     Query Match
Best Local S
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J. Virol. 73:5777-5786(1999).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR (TAR) RNA ELEMENT AND
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99292873; PubMed-10364329; Bieniasz P.D., Grdina T.A., Bogerd H.P., Cullen B.R.; "Analysis of the effect of natural sequence variation in Tat and in cyclin T on the formation and RNA binding properties of Tat-cyclin T
                                                                                                                                                                                                                          17 OPKTACIN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTS 75
                                                                                                      Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                   3;
                                                                                                                                                                       Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (isolate ROD) (HIV-2).
                                                                                                                                                                      30.9%; Score 170.5; DB 1; Length 47.9%; Pred. No. 6.5e-10; live 8; Mismatches 26; Indels
                                                                                                                                130 AA; 14383 MW; 1AA63DE911DD9DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome organization and transactivation of the human immunodeficiency virus type 2."; Nature 326:662-669(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS OF CYS-50, AND INTERACTION WITH CYCLIN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 2 (isolate ROD) (
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1AT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                                                         130 AA
 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87173056; PubMed-3031510;
                                  PIR; F33943; TNLJST.
HIV; M3113; TAT$2ST.
HIVERPLO; IPROO1831; HIV_TAt.
Pfam; PF00539; Tat; 1.
PRINTS; PRO0055; HIVTATDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: BINDS CYCLIN T1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; MIS390; AAB00768.1; -. EMBL; X05291; CAA28912.1; -. PIR; E26262; TWLJG2.
HIV; MIS390; TAT$2ROD.
                        EMBL; M31113; AAB01356.1; -.
                                                                                                                                                                                    Local Similarity 47.9 nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                       103 TRTGNSOPEKK 113
                                                                                                                                                                                                                                                                            76 QSKGEPTGPKE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11720;
                                                                                                                                                                                                                                                                                                                                                                      TAT_HV2RO
P04605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alizon M.;
                                                                                                                                SEQUENCE
                                                                                                                                                                       Query Match
                                                                                                                                                                                                Matches
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-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                          17 QPKTACTN-CYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQGSQTH-----QVSLS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Franscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                           13;
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50 C->S: LOSS OF BINDING TO CYCLIN T. 14720 MW; 3B0EB94021644CE7 CRC64;
                                                                                                     29.6%; Score 163.5; DB 1; Length 130; 42.7%; Pred. No. 3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91170959; PubMed-2005437;
Tristem M., Hill F., Karpas A.;
"Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type 2 proviral clone (HIV-2CAM2).";
J. Gen. Virol. 72:721-724(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                         24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 133 AA; 14850 MW; CFAB978387B3C1FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.38; Scor V 43.88; Pred. No. 4...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AA.
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                   103 TRIGDSOPTKKOKKTVEATVET 124
                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00055; HIVTATDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; I38475; TNLJCA.
InterPro; IPR001831; HIV_Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D00835; BAA00714.1; -.
                                                                                                                                                                                                                                                                                                                  71 -----KQPTSQSKGEPTGPKET
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00539; Tat; 1
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Search completed: August 26, 2002, 08:15:43
Job time: 347 sec
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"Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of
'neuro-AIDS', Which showed excellent growth in macrophages.";
Nucleic Acids Res. 18:6142-6142(1990).
-i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIRR
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MEDLINE-89184631; PubMed-2467304;
Kuehnel H., von Briesen H., Dietrich U., Adamski M., Mix D.,
Blesert L., Kreutz R., Immelmann A., Henco K., Meichsner C.,
Andreesen R., Gelderblom H., Ruebsamen Waigmann H.;
"Molecular cloning of two west African human immunodeficiency virus
type 2 isolates that replicate well in macrophages: a Gambian
isolate, from a patient with neurologic acquired immunodeficiency
syndrome, and a highly divergent Ghanian isolate, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Activator; RNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 2 (isolate D194) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.2%; Score 161; DB 1; Length 13
33.9%; Pred. No. 5.3e-09;
ive 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA; 14597 MW; 1A659CB2F933C537 CRC64;
                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1997 (Rel. 35, Last annotation update)
TAT protein (Transactivating regulatory protein).
                                                                                                                                                                           130 AA.
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-91045094; Pubmed-2235509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIVTATDOMAIN
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Pfam; PF00539; Tat; 1.
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                                                                                                                                                                           STANDARD;
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PIR; S12157; S12157.
HIV; J04542; TAT$2D194.
                                                 106 TRIRNSQPAKKQK 118
78
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Matches 39; Conserv
-----KQPTSQSK
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                                                                                                                                                                        TAT_HV2D1
P17759;
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71
                                                                                                                                              TAT_HV2D1

AC D1-AU
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RT SYOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ranscription regulation; Activator; RNA-binding; Nuclear protein;
17 OPKTACIN-CYCKKCCFHCOVCFITAALGISYGRKKRRORRRPPQGSQTHQVSLSKOP
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                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus (Mm142-83 isolate) (SIV-MAC).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AA; 14545 MW; DA133BC4BAB7F521 CRC64;
                                                                                                                                                                                                                                                     TAT protein (Transactivating regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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50.0%; Pred. No. 7.3e-09;
iive 10; Mismatches 16
                                                                                                                                                                                  (Rel. 09, Created)
(Rel. 09, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
-!- MISCELLANEOUS: THIS IS A MACAQUE ISOLATE.
                                                                                                                                     130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87287230; PubMed-3649576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y00277; CAB46521.1; -. PIR; F28887; TNLJG3.
HIV; M16403; TAT$MM142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                     STANDARD;
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01-NOV-1988 (
16-OCT-2001 (
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Best Local Simi
Matches 29;
                                                                                                                                TAT_SIVM1 P05911;
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARIY).
EMBL; D86069; BAA13000.1; --
INTERPRO; IPR01831; HIV_TAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90101366; Pubmed-1688473; Cloyd M.W., Moore B.E.; Spectrum of Biological Properties of Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; RNA-binding; Transcription regulation.
9865 MW; 4DDC56C1CE269115 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                               Q73370
093199
Q9W9E3
Q9WJW7
                                                              077688
P90265
Q04191
O40219
                                                                                                                 0902S7
011405
092895
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                                                                                                                                                                                Q9WJV2
Q99BV9
Q75758
Q92902
Q72990
                                                                                                                                                                                                                                                                                                 Q9WJV9
Q04192
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PRINTS; PR00055; HIVTATDOMAIN.
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91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 174:103-116(1990)
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Activator; Nuclear
SEQUENCE 86 AA;
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Best Local Similarity
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(HIV-1) Isolates
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                                                                                                                                                       074087
 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    August 26, 2002, 08:14:57; Search time 86.53 Seconds (Without alignments) 189.929.Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 ~ 2000 Compugen Ltd.
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                                                                                                                                                                                                                                562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
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Q900A7
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099BW0
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_invertebrate:*
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sp_organelle:*
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length: 2000000000
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Post-processing:

Database

Minimum DB seq Maximum DB seq

Title: Perfect score: Sequence:

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Run on:

Scoring table:

Searched:

simian-huma

056318

444 4445 4443 4443

Score

Š. Result

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EMBL; AF256210; AAG16839.1; -
EMBL; AF256209; AAG16831.1; -
InterPro; IPR001831; HIV_Tat.
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                                                                                           PRELIMINARY;
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clinical outcome.
Submitted (NOV-20
                                                                                                                                                                               01-JUN-2001
01-DEC-2001
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                                                                                                                    099BV4;
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                            RESULT
Q99BV4
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Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
"Recovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
Virology 213:80-86(1995)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95074930; PubMed-7983770;
Fang H., Pincus S.H.;
"Unique insertion sequence and pattern of CD4 expression in variants selected with immunotoxins from human immunodeficiency virus type I-infected T cells.";
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                                                                                       Spontaneous activation of human immunodeficiency virus type 1 in an
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   5; Indels
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
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J. Virol. 59:284-291(1986).
EMBL, AF070521; AAC28449.1; -.
EMBL; U26842; AAB60575.1; -.
SEQUENCE 86 AA; 9845 MW; 26B2281979769110 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 3.9e-47;
3; Mismatches 5;
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   Mismatches
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90.7%;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
TAT PROTEIN.
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Best Local Similarity 90.7
Matches 78; Conservative
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Fang H., Pincus S.H.;
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79;
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STRAIN=P12.2; Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J., Froebel K.S.; "The natural history of pediatric HIV infection suggests an association between the specificity of the cytotoxic T cells and
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-:- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND PROMOTER (BY SIMILARITY).

EMBL, AF324449, AAK14291.1;

InterPro: IPR001831; HIV_Tat.

Pfam: PF00559; Tat.

PRINTS; PR00055; HIVTATDOMAIN.
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MEDLINE=20457217; PubMed=11000225;
Yuste B., Lopez-Galindez C., Domingo E.;
Yuste B., Lopez-Galindez C., Domingo E.;
Yuste B., Lopez-Galindez C., Domingo E.;
J. Virol. 74:9546-9552(2000).
-!- FOWCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).
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SEQUENCE 86 AA; 9842 MW; 60C7F0727C482F49 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 6.8e-47;
3; Mismatches 6;
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86 AA.
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Oelrichs R.B., McPhee D.A., Deacon N.J.;
Oelrichs R.B., McPhee D.A., Deacon N.J.;
Deacoing and full-length sequence of two Australian HIV-1
primary clinical isolates with distinct cellular tropism and
cytopathicity.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
PROMOTER (BY SIMILARITY):
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EMBL, AF042100, AAD03194.1;
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InterProj. PROMOTER (11/2) ---
InterProj. PROMOTER (11/2) ---
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INTERPROJ. PR
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PRINTS; PR00055; HIVTATDOMAIN.
Activator; Nuclear protein; RNA-binding; Transcription regulation.
SEQUENCE 101 AA: 11425 MW; 1A1E45C93960630E CRC64;
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                                                                                                                                                         DB 15; Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPhee D.A.;
Repid full-length genomic sequencing of two cytopathically
heterogeneous Australian primary HIV-1 isolates.";
J. Biomed. Sci. 7:128-135(2000).
                                                                                                                                                    Score 446; DB 15; Length 1
Pred. No. 8e-47;
2; Mismatches 7; Indels
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MEDLINE-20219736; PubMed-10754387;
Oeliichs R.B., Lawson V.A., Coates K.M., Chatfield C.,
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 1.1e-46;
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89.5%;
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(TrEMBLrel. 08, I
(TrEMBLrel. 19, I
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89.7%;
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Best Local Similarity
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Best Local Similarity
Matches 78; Conserv
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01-DEC-2001
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STRAIN-P12.1;
Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,
Froebel K.S.;
                                                                                                                                                                                                                                                                                                                                              Clinical outcome.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGILATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

EMBL, AF3244448; AAK14290.1;
-InterPro; IRR001831; HIV_Tat.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND PROMOTER (BY SIMILARITY).
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Yuste E., Lopez-Galindez C., Domingo E.;
"Unusual Distribution of Mutations Associated with Serial Bottleneck
Passages of Human Immunodeficiency Virus Type I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRPPQ 60
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PRIMITS: PROD055; HIVTATDOMAIN.
ACTIVATOR: Nuclear protein; RNA-binding; Transcription regulation.
ACTIVATOR: R6 AA: 9828 MW; C1C6E1727D928438 CRC64;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
(TRANSACTIVATING REGULATORY PROTEIN).
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(Tremblrel. 19, Last annotation update)
(TRANSACTIVATING REGULATORY PROTEIN).
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NCBL_TaxID-11676;
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NCBI_TaxID=11676;
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Pred. No. 1.6e-46;
86 AA
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                                         Created)
PRT;
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01-JUN-2001
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STRAIN-SHIV-4, AND HXBC2;
STRAIN-SHIV-4, AND HXBC2;
Relmann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
Sodroski J., Letvin N.L.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: TRANSCRIPTIONAL RESULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Infection of cynomolgus monkeys With a chimeric HIV-1/SIVmac virus
that expresses the HIV-1 envelope glycoproteins.";
J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
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                                                                                                                                                                                                            RNA-binding; Transcription regulation.
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                                                                                                                                                                                                                                                                                                         Length 101
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Pred. No. 1.9e-46;
3; Mismatches 7;
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SEQUENCE FROM N.A.
STRAIN-SHIV-4, AND HXBC2;
MEDLINE-92309177; PubMed-1613662;
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                                                                                                                                                                                                                 Activator; Nuclear protein; RN
SEQUENCE 101 AA; 11453 MW;
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(TrEMBLrel. 06, I
(TrEMBLrel. 19, I
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88.5%;
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Best Local Similarity 88.5
Matches 77; Conservative
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01-JUN-1998
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SEQUENCE
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Score 442; DB 15; Length 86; Pred. No. 2.1e-46;

80.1%;

Query Match Best Local Similarity

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Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The natural history of pediatric HIV infection suggests an association between the specificity of the cytotoxic T cells and clinical outcome.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                        1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
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EMBL, AFS14446; AAK14288.1; -

InterPro; IPR001831; HUV_Tat.

Pfam: PF00539; Tat; 1.

Pfam: PF00555; HIVTATDOMAIN.

ACLIVALOT; NUClear DOMALN.

SEQUENCE 101 AA: 11517 MW; 03AB48CCC28C9DE2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 3.3e-46;
3; Mismatches 7;
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              Mismatches
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              Conservative
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Best Local Similarity
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Aldhous M.C., Schwager M., Mok J.T.Q., Yirrell D.L., Leigh Brown A.J.,
Froebel K.S.;
                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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Froebel K.S.; "The natural history of pediatric HIV infection suggests an association between the specificity of the cytotoxic T cells and
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Pred. No. 3.7e-46;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                               7; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACIIVATING RECULATORY PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 3.7e-46;
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88.4%;
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89.5%;
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Best Local Similarity 88.4
Matches 76; Conservative
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Best Local Simi
Matches 77;
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Q99BV3
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GSQTHQVSLSKQPTSQSKGEPTGPKE 86

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Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,
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Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J., Froebel K.S.;
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSTVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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SEQUENCE 86 AA; 9725 MW; 3ALC9D514983A7A8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clinical outcome.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Pred. No. 4.8e-46;
3; Mismatches 7;
                                                                                                                                            86 AA.
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 19, Last ann
                                                                                                                                                                                                   Created)
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61 SSQTHQVSLSKQPTSQPRGDPTGPKE 86
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InterPro; IPR001831; HIV_Tat.
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01-JUN-2001
01-DEC-2001
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Best Local Simi
Matches 76;
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01-DEC-2001
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: TRANSCRIPTIONAL REGULANDRY THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROWOTER (BY SIMILARITY).

PROWOTER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-MBC925;
Oelrichs R.B., McPhee D.A., Deacon N.J.;
aliological cloning and full-length sequence of two Australian HIV-1 primary clinical isolates with distinct cellular tropism and
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                                                                                                                                    Gaps
                                                                                                                                                         1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                                                     1 MEPUDPRIEDWRHPGSQPKTACTNCYCKKCCFHCQVCFTTKALGISYGRKKRRQRRTTPP 60
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MEDLINE-20219736; PubMed-10754387;
Oelrichs R.B., Lawson V.A., Coates K.M., Chatfield C., Deacon N.J.,
                  EMBL; AF334442; AAK14285.1; '.
InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
ACLIVATOR; NUCLEAR PROFESS, RNA binding; Transcription regulation.
SEQUENCE 86 AA; 9803 MW; 9B0D8E524AEC1B0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; RNA-binding; Transcription regulation.
101 AA; 11576 MW; 93352253792B3FB2 CRC64;
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                                                                                                                                    7; Indels
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                                                                                                             Length
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses: Retroid viruses: Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 5.7e-46;
4; Mismatches 7;
                                                                                                            Score 439; DB 15;
Pred. No. 4.8e-46;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                    101 AA.
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InterPro, IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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PROMOTER (BY SIMILARITY).
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89.5%;
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87.4%;
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Matches 77; Conservative
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Best Local Similarity
Matches 76; Conservat
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01-DEC-2001
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activator; Nuclear protein; RNA-binding; Transcription regulation.
SEQUENCE 101 AA; 11512 MW; 440B807D4F48738E CRC64;
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MEDLINE-96186751; PubMed-8627800;
Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Rac;
Lin W., Monteflori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                           Last sequence update)
Last annotation update)
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NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=57667;
                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Pred. No. 5.7e-46;
8; Mismatches 5;
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01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                           PRT;
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EMBL; AF042105; AAD03236.1; -.
InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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ilarity 85.1%;
Conservative,
                                           PRELIMINARY;
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Best Local Similarity
Matches 74; Conserv
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RESULT 15
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STRAIN-P6.3;
Aldhous M.C., Schwager M., Mok J.Y.Q., Yirrell D.L., Leigh Brown A.J.,
Froebel K.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER BY SIMILARITY).

EMBL, AF324444; AAK14287.1; ...
Interpro; IPR001831; HIV_Tat.
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SEQUENCE 101 AA; 11615 MW; 5F80827F08100F03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The natural history of pediatric HIV infection suggests an association between the specificity of the cytotoxic T cells and
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MEDLINE=20564795; PubMed=11112486;
Salminen M.O., Ehrenberg P.K., Mascola J.R., Dayhoff D.E., M Blake B., Louder M., Hegerich S., Polonis V.R., Birx D.L., R McCutchan F.E., Michael N.L., "Construction and biological characterization of infectious clones of HIV-1 subtypes B and E (CRF01_AE) generated by the polymerase chain reaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clinical outcome."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
far PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 7.6e-46;
4; Mismatches 7;
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ilarity 87.4%;
Conservative
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                                                                       PRELIMINARY;
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Best Local Similarity
Matches 76; Conserv
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Octions R.B., McPhee D.A., Deacon N.J.;
"Genomic sequence of HIV-1 from four members of the Sydney Blood Bank Cohort of long term non-progressors."

Cohort of long term non-progressors."

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-: FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
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SEQUENCE 101 AA; 11509 MW; 974357617DBDEF30 CRC64;
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TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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EMBL; AF038398; AA89963.1; -.
InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
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InterPro; IPR001831; HIV_Tat.
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TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
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Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
Watanavecradej V., Pando M., Negrete M., Russell K.L., Sanchez J.,
Birx D.L., Andrade R., Vinoles J., McCutchan F.E.;
"Diverse BF Recombinants have spread widely since the introduction of
AIDS 0:00(2001).
Blake B., Louder M., Hegerich S., Polonis V.R., Birx D.L., Robb M.L., McCutchan F.E., Michael N.L.;
McCutchan F.E., Michael N.L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATION RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).
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SEQUENCE 101 AA; 11572 MW; E1F97B5162E3C813 CRC64;
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Pred. No. 1e-45;
4; Mismatches 7; Indels
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SEQUENCE 101 AA; 11478 MW; 34432B8FD16F5DFC CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 1e-45;
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PRM; PF00539; Tat; 1.
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Best Local Similarity 87.4%;
Matches 76; Conservative
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TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).
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"Nucleotide sequence of a Cambridge isolate of human immunodeficiency
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                                                                                                                                                                                                                                                                                 Olivares I., Casado C., Iglesias-Ussel M.D., Dietrich U.,
Lopez-galindez C.;
"Complete sequence of an infectious molecular clone derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding; Transcription regulation.
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SEQUENCE 101 AA; 11430 MW; B76CF7B13E60C3EF CRC64;
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                                                                                                                                      Lopez-galindez C.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 19, Last annotation update)
(TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 2.3e-45;
3; Mismatches 8;
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MEDLINE-99085865; Pubmed-9870318;
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SEQUENCE 101 AA; 11512 MW;
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InterPro; IPR001831; HIV_TAt.
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                                                                                                                                                                                                                                                                                                                                                           Spanish HIV type 1 isolate.";
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Best Local Similarity 87.4%;
Matches 76; Conservative
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SEQUENCE FROM N.A. Rettz M., Popovic M., Gartner S., Gallo R., Reed-Connole
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR FRONCIER (BY SIMILARITY).

EMBL: U21135; AAC32297.1; --
InterPro, IPR001831; HIV_Tat.

Pfam; PF00559; Tat; 1.
                                                                             Gaps
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                                                                                                                   MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ 60
                                                                                                                                        1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRPPQ 60
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Pred. No. 2.3e-45;
5; Mismatches 7; Indels (
                                     Length 101;
                                                                             Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                   Score 434; DB 15;
Pred. No. 2.3e-45;
5; Mismatches 7;
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SSKTHQASLSKQPASQFQGDPTGPKES 87
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SEQUENCE 101 AA; 11702 MW;
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86.2%;
                                   78.6%;
85.1%;
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Best Local Similarity 86.2
Matches 75, Conservative
                                                                             Conservative
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                                                      Similarity
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01-NOV-1996 (
01-NOV-1996 (
01-JUN-2001 (
TAT PROTEIN (
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01-MAY-1997 (
01-DEC-2001 (
                                   Query Match
Best Local Simi
Matches 74;
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P90265;
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P90265
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004191
1D 000
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Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TAT IS AN EFFECTOR OF AN AUTOSTIMULATORY PATHWAY THROUGH
INTERACTION WITH A POSITIVE CONTROL ELEMENT, THE TRANS-ACTIVATING
RESPONSIVE SEQUENCE (TAR)
-!- MISCELLANEOUS: DELETION MUTANTS IN THE TAT GENE ARE INCAPABLE OF
PROLIFIC REPLICATION AND EXHIBIT NO CYTOPATHIC EFFECTS IN T4+ CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin M.A., Peden K.W.; "Construction of a stable full-length macrophage-"Construction and characterization of a stable full-length macrophage-tropic HIV type 1 molecular clone that directs the production of high titers of progeny virions.";
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Theodore T.S., Englund G., Buckler-White A., Buckler C.E.,
Martin M.A., Peden K.W.C.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER (BY SIMILARITY).
EMBL, AF004394, AAB64167.1;
-InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 11
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
(TRANSACTIVATING REGULATORY PROTEIN).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 434; DB 15;
Pred. No. 2.3e-45;
5; Mismatches 7;
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InterPro; IPR001831; HIV_Tat.
Pfan; PF00539; Tat; 1.
PRINTS; PR00055; HIVTATDOMAIN.
Transcription regulation; AIDS.
SEQUENCE 101 AA; 11547 MW; A'
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Activator; Nuclear protein; RN
SEQUENCE 101 AA; 11632 MW;
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Best Local Similarity 85.1%;
Matches 74; Conservative
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SEQUENCE FROM N.A.
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01-DEC-2001 (
TAT PROTEIN (
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Beaver B.;
Submitted
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Length 101;

DB 15;

Score 433;

78.48;

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01-NOV-1998
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                                                1 MEPVDPRLEPWKHPGSQPRTACNNCYCKKCCFHCQVCFTRKGLGISYGRKKRRQRRRTPQ 60
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ARCH054;
STRAIN-ARCH054;
Matanaveeradej V., Pando M., Negrete M., Russell K.L., Sanchez J.,
Birx D.L., Andrade R., Vinoles J., McCutchan F.E.;
"Diverse BF Recombinants have spread widely since the introduction
                                     1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRRPPQ
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                   Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                     Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian-Human immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                           Score 433; DB 15; 1
Pred. No. 3.1e-45;
7; Mismatches 7;
Pred. No. 3.1e-45;
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                                                                                                                                         PRT;
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                                                                         61 GSQTHQVSLSKQPTSQSKGEPTGPKET
                                                                                   78.4%;
83.9%;
                                                                                                                                                          (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
         85.1%;
                                                                                                                                                                                                                                                                                                     into South America.";
                                                                                                                                                                                                                                                                                                                                                 Similarity 85.1
'4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                   01-DEC-2001
01-DEC-2001
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01-DEC-2001
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          Best Local
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                  Matches
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-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMBL; U89134; AAC57424.1; -- EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMTS; PR00055; HIVTATDOWAIN.
Activator; Nuclear protein; RNA-binding; Transcription regulation.
SEQUENCE 101 AA; 11508 MW; A58C2FBA1E2482E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; RNA-binding; Transcription regulation.
102 AA; 11745 MW; E9DCD9BDD09970C0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Pred. No. 4 1e-45;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 433; DB 15;
Pred. No. 3.1e-45;
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DSKTHQVSLPQQPSSQPRGDPTGPKES 87
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InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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08,
19,
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ilarity 87.2%;
Conservative
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Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  102 AA;
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Best Local Similarity
Matches 75; Conserv
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1 MEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITAALGISYGRKKRRQRRPPQ 60
                                                                                                                                                                                                                                                                                                     DSOTHOVSLSKOPASOPRGDPTGPKES
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Matches 74; Conserv
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: TRANSCRIPTIONAL FEGULATOR THAT ACTS BY BINDING TO THE TRANS-CATIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).
EMBL; U43096; AAA866250.1;
INTERPIO; IPR001831; HIV_Tat.
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-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Groenink M., Fouchier R.A.M., De Goede R.E.Y., de Wolf F., Catuters R.A., Cuppers H.T.M., Huisman H.G., Tersmette M.; Phenotypic heterogeneity in a panel of infectious molecular human immunodeficiencey virus type 1 clones derived from a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activator; Nuclear protein; RNA-binding; Transcription regulation.
SEQUENCE 101 AA; 11501 MW; 00BA1B72DD916FE6 CRC64;
                                                                                                                                                                                                                                                "Analysis of the envelope region of the highly divergent HIV-2ALT stoolate extends the known range of variability within the primate immunodeficiency viruses."; AIDS Res. Hum. Retroviruses 8:1619-1629(1992).
                                                                                                                                                                                                                     Kreutz R., Dietrich U., Kuhnel H., Nieselt-Struwe K., Eigen M.,
Rubsamen-Waigmann H.;
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Pred. No. 4.1e-45;
5; Mismatches 8; Indels (
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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 101 AA.
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                                Created)
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 PRT;
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                                                                                                                                                                                       STRAIN-D31;
MEDLINE-93090480; Pubmed-1457208;
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85.1%;
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 PRELIMINARY;
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Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
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01-NOV-1996 (
01-DEC-2001 (
Q74810
Q74810;
01-NOV-1996
                                             01-NOV-1996
01-DEC-2001
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Q80270
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ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LIR
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Activator; Nuclear protein; RNA-binding; Transcription regulation.
SEQUENCE 101 AA; 11525 MW; 8B1A9AA50D4F656F CRC64;
                                       PROMOTER (BY SIMILARITY).
EMBL, M64491, AAA45079.1; ..
InterPro; IPR001831; HIV_Tat.
Pfam; PF00539; Tat; 1.
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Gaps . 0 Length 101; Indels Score 431; DB 15; Pred, No. 5.4e-45; 4; Mismatches 78.1%; 85.1%; Conservative

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1 MEPUDPKLEPWKHPGSQPKTACNNCYCKKCCFHCQVCFTKKGLGISYGRKKRRQRRRAPQ 60

61 GSQTHQVSLSKQPTSQSKGEPTGPKET 87

Search completed: August 26, 2002, 08:14:58 Job time: 386 sec

	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
OM protein - pro	OM protein - protein search, using sw model	
Run on:	August 26, 2002, 08:08:31; Search time 99.16 Seconds (without alignments) 338.284 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-509-239-13 1688 1 MGGKWSKSSVVGWPTVRERMQSRGDPTGPKETSGHHHHHH 302	
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	747574 seqs, 111073796 residues	
Total number of	Total number of hits satisfying chosen parameters: 747574	
Minimum DB seq 1 Maximum DB seq 1	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing:	Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries	
Database :	A_Geneseq_032802:*	

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7: /SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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176: /SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
187: /SIDS1/gcddata/hold-geneseq/geneseqp-embl/AA1999.DAT:\*
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211: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:\*
212: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	A representative H	Amino acid sequenc	Amino acid sequenc	A representative L	Amino acid sequenc	A representative H	Amino acid sequenc	A representative L	A representative H	Amino acid sequenc	A representative L
QI	AAY02351	AAG63233	AAG63235	AAY02355	AAG63237	AAY02357	AAG63239	AAY02353	AAY02349	AAG63231	AAY02352
	302 20	302 22	411 22	413 20	•	302 20				215 22	
% Ouery Match Length DB	100.0	100.0	100.0	100.0	100.0	99.2	99.2	99.2	67.5	67.5	67.5
Score	1688	1688	1688	1688	1688	1675	1675	1675	1139.5	1139.5	1139.5
Result No.	1	7	ო	4	ហ	Q	7	ω	σ	10	11

Amino acid sequenc	A representative L	Amino acid sequenc		rotei	HIV-1 nef protein.		Sequence of E' pro	of	ш	HIV-1 jrfl Nef pro	1n 6	(ATCC	HIV-1 jrfl Nef (G2	strai	Human tPA leader p		HIV-1 non-subtype			O	HIV-1 non-subtype	Sequence deduced f	_				_			HIV-1 non-subtype	HIV isolate LAV.MA	Sedneuce eucoded p	HIV-1 strain YBF30
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34	154	136	795	393	54	126		23	.79	096	.13	668	162	362	161			69	191	69	359	107	364	356	9362	365	366	357	358	9360	866	99	481
AAG6323	AAY 023	AAG6323	AAY5079	AAR3889	AAB1005	AAW8932	AAP61515	AAP6042	AAW9017	AAE0496	<b>AAW531</b>	AAY7729	AAE0496	<b>AAR1226</b>	AAE0496	AAE0496	AAB6936	AAB861	AAB693	AAP8185	AAB69359	AAR08407	AAB69364	AAB693	AAB693	AAB69365	AAB6936	AAB693	AAB6935	AAB693	AAW7299	AAP8186	AAW684
22	20	22	21	14	21	20	7	~	20	22	13	21	22	17	22	22	21	C)	21	6	21	11	21	21	21	21	21	71	21	21	19	σ	13
324	326	326	206	206	206	206	206	216	206	216	210	210	217	210	237	237	206	3025	206	206	207	207	207	208	219	217	207	207	206	206	209	209	212
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		67	99	99			65				29				57	57	26	56	55	54	53	53	53	53	53	25	25	25	5	20	49	49	47
1139.5	an.	an.	$\overline{}$	1116	~	1114	1111	1107	1092	1011	697	666	966	983	978	896	952	948.5	934		910.5	903.5	901.5	901.5	895.5	893.5	885.5	878.5	867	860	834.5	31	796
12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY0235	RESULI I AAY02351
1	AAY02351 standard; Protein; 302 AA.
×	
AC	AAY02351;
×	
DŢ	09-JUL-1999 (first entry)
×	
DE	A representative HIV-1 Nef-Tat-His protein.
×	
Κ¥	HIV nef gene; fusion protein; HIV nef gene; Nef protein; Tat protein;
Κ¥	vaccine; HIV infection; protein D.
X,	
SO	Synthetic.
SO	Human immunodeficiency virus type 1.
×	
PN	WO9916884-A1.
×	
PD	08-APR-1999.
×	
ΡF	17-SEP-1998; 98WO-EP06040.
×	
PR	26-SEP-1997; 97GB-0020585.
YY	
PA	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
××	
PI	Bruck C, Godart SAG, Marchand M;
DR	WPT: 1999-302282/25
20	N-DSOB: AAX35687
×	
PŢ	HIV Tat or Nef protein linked to a fusion partner
XX	•
bS	Disclosure; Fig 2; 66pp; English.

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31-JAN-2000; 2000GB-0002200
                                                                                                                       302 AA;
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      The present sequence represents a representative HIV-1 Nef-Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                               LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH 240
                                                                                                                                                                                                                                               FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                       COVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH 300
                                                                                        Gaps
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                                                                                                      1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
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linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
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                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a His-tagged Nef-Tat linked protein of
                                                                       Score 1688; DB 20; Length 302; Pred. No. 8.4e-156;
                                                                                                                                                                                                                                                                                                                                                                                              HIV; nef gene; tat gene; vaccine; gp120 gene; HIV viral load
                                                                                Pred. No. 8.4
Mismatches
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                                                                      100.0%;
llarity 100.0%;
Conservative 0;
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2000GB-0009336.
2000GB-0013806.
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                                                                               Best Local Similarity
Matches 302; Conser
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14-APR-2000;
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The present sequence represents a His-tagged Nef-Tat linked protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylatactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The act in vaccine she HIV viral load in HIV infected humans and results in amintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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protein or polynucleotide for the manufacture of a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1688; DB 22; Best Local Similarity 100.0%; Pred. No. 8.4e-156; Matches 302; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                       Disclosure; Fig 1; 90pp; English.
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Human immunodeficiency virus
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HIV infection; protein

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vaccine;
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                                                                                                                                                                        The present sequence represents a His-tagged Nef-Tat linked protein of HIV, with a lipidation signal sequence (LipoD) which is removed after processing and a Proto fusion partner. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV 9D120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with 9p120 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat
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                                                                                                              New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef
linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20
protein or polynucleotide for the manufacture of a vaccine -
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Pred. No. 1.3e-155;
Mismatches 0;
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                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                                                                        English.
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2000GB-0009336.
2000GB-0013806.
2000WO-EP05998.
                                                                                                                                                      Disclosure; Fig 1; 90pp;
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N-PSDB; AAH42879.
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14-APR-2000;
06-JUN-2000;
                     28-JUN-2000;
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The present sequence represents a fusion protein comprising LipoD-HIV-1 Tat. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.
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                                                                                                                                                                                                                                                                                                                                    HIV Tat or Nef protein linked to a fusion partner
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                          type
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                      virus
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Synthetic.
Human immunodeficiency
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                                                           WO9916884-A1
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                                                                                               08-APR-1999
                                                                                                                                                                                                                                            Bruck C,
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AAG63237
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The present sequence represents a His-tagged ProtD-Nef-Tat fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gp120 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gp120 in the treatment and prevention of HIV. The accordance the HIV Intal load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gp120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 mggkwskssvvgwptvrermrraepaadgvgaasrdlekhgaitssntaatnaacawlea 171
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                                                                                                                                                                                                                                                                                                                                         New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 413;
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Pred. No. 1.3e-155;
; Mismatches 0;
                                                                         /note- "ProtD fusion partner"
                                                                                                                                                                                                                                                    SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                 Location/Qualifiers 1..111
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 90pp; English
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100.0%;
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2000GB-0013806.
2000WO-EP05998.
                         Human immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                     WO200154719-A2
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06-JUN-2000;
28-JUN-2000;
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Best Local Simil
Matches 302; C
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The present sequence represents a representative HIV-1 mutant Tat-His protein. The protein is used in the creation of the fusion proteins of the invention, in conjunction with a fusion partner (e.g. protein D). The specification also describes fusion proteins, comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSOPKTACTNCYCKKCCFH 240
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                                                                                                                                                                                                                                                                          protein; Tat protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%; Score 1675; DB 20; Length 302; 99.0%; Pred. No. 1.5e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                          gene; Nef
                                                                                                                                                                                                                     A representative HIV-1 mutant Tat-His protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                       ; fusion protein; HIV nef infection; protein D.
                                                    AAY02357 standard; Protein; 302 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 66pp; English
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-302282/25
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                                                                                                                                                                                                                                                                             gene;
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AAG63239;

AAG63239

02-AUG-2001

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The present sequence represents a fusion protein comprising LipoD-HIV-1 Tat-His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Nef protein. The fusion protein can be used in a vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                       protein; Tat protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 2.4e-154;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                                                                                                                    fusion protein; HIV nef gene; Nef infection; protein D.
                                                                                                                                                                                                                                                                                                                      representative LipoD-Tat-His fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                                          AAY02353 standard; Protein; 411 AA.
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llarity 99.7%;
Conservative (
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                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-302282/25.
N-PSDB; AAX35689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1998;
                                                                                                                                                                                                                                                                                        09-JUL-1999
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                                                                                                                                1.1
hh 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim:
Matches 301;
                                                                                                              HH 302
                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruck C,
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                                                                                                              301
                                                                                                                                             301
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                                                                                                                                                                                            RESULT
AAY02353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a His-tagged mutant His protein of HIV. The protein is expressed in the yeast Pichia pastoris, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or Nef
gp120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEBEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                        Amino acid sequence of a His-tagged mutant His protein of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New use of a human immunodeficiency virus (HIV) Tat, or Nef, linked to Tat (Nef-Tat) protein or polynucleotide and an HIV protein or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 302;
                                                                                                                                                                                                        HIV; nef gene; tat gene; vaccine; gpl20 gene; HIV viral load.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1675; DB 22;
Pred. No. 1.5e-154;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 90pp; English.
                                                                           AAG63239 standard; Protein; 302
                                                                                                                                                                                                                                      Synthetic.
Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.2%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2000, 2000GB-0002200.
14-ARR-2000, 2000GB-0009336.
06-JUN-2000, 2000GB-001396.
28-JUN-2000, 2000WO-EP05998.
                                                                                                                                                                                                                                                                                                                                                29-JAN-2001; 2001WO-EP00944
                                                                                                                                          (first entry)
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N-PSDB; AAH42883.
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Best Local Similarity
Matches 299; Conserv
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Sequence

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QY         181 LEWREDSRLAFHHVARELHPEVFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH           Db         181 lewrfdSrlafhhvarelhpeyfknc           QY         241 CQVCFITKALGISYGRKKRRQPRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH           Db         207           QY         301 HH 302           Db         214 hh 215	RESULT 10 AAG63231 ID AAG63231 XX AC AAG63231: XX AC AAG63231: XX DT 01-OCT-2001 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX	Synthetic.  Human immunodeficiency virus.  W0200154719-A2.  02-AUG-2001.  29-JAN-2001; 2001W0-EP00944.			protein is expressed in the yeast Pichia pastoris, and is used to protein is expressed in the yeast Pichia pastoris, and is used to compound the produce the vaccine of the invention. The specification describes computed the Year and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or compared with gpl20 in the treatment and prevention of HIV. The compound in the treatment and prevention of HIV. The compared vaccine reduces the HIV viral load in HIV infected humans and results compared to the properties of the properties of compared the Viral load in HIV infected humans and results compared to vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.	Ouery Match 67.5%; Score 1139.5; DB 22; Length 215; Best Local Similarity 71.2%; Pred. No. 1.2e-102; Matches 215; Conservative 0; Mismatches 0; Indels 87; Gaps Oy 1 MGGKWSKSSVVGWPTVRERMRREPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
DD 290 lewrfdsrlafhhvarelhpeyfknctsepvdprlepwkhpgsqpktactncyckkcofn 349 Qy 241 CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDFTGPKETSGHHHH 300	RESULT 9 AAY02349 ID AAY02349 XX XX AAY02349; XX AY DT 09-JUL-1999 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX	Synthetic. Human immunoo WO9916884-Al. 08-APR-1999.	SMITHKLINE BEECHAM BIOLOGIC Godart SAG, Marchand M: 99-302282/25.	HIV Tat or Net protein linked to a rusion partner  XX  XX  XX  Disclosure; Fig 2; 66pp; English.  CC  The present sequence represents a representative HIV-1 Nef-His protein.  CC  The protein is used in the creation of the fusion proteins of  CC  The invention, in conjunction with a fusion partner (e.g. protein D).  CC  The specification also describes fusion proteins comprising HIV-1 Tat  CC  CC  The fusion protein can be used in a vaccine to prevent.HIV	Sue Jata Tata	Oy 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTGGY 120

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                                                                                                                                                                             the represents a His-tagged Nef protein of HIV. The sed in the yeast Pichia pastoris, and is used to be of the invention. The specification describes in HIV Nef, or Nef-Tat; and HIV gpl20 in the accine. The vaccine is used for the prophylactic or zation of humans against HIV. Tat, Nef or Nef-Tat act 120 in the treatment and prevention of HIV. The HIV viral load in HIV infected humans and results of CD4+ levels over those levels found in the absence the HIV Tat, Nef or Nef-Tat and HIV gpl20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1139.5; DB 22; Length 215;
Pred. No. 1.2e-102;
0; Mismatches 0; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodeficiency virus (HIV) Tat, or Nef, or Nef
Tat) protein or polynucleotide and an HIV gpl20
eotide for the manufacture of a vaccine -
                                                                                                                           90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.58;
71.28;
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QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                            316 ----
                                                                                                                                             301 HH 302
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                                                                                                                                                                                                                             AAG63234;
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                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a fusion protein comprising LipoD-HIV-1 Nef-His. The protein is exemplifies the fusion proteins of the invention. The specification also describes fusion proteins comprising HIV-1 Tat protein. The fusion protein can be used in a vaccine to prevent HIV infection.
                  120
                                                                      240
                                                                                                         300
                                    180
                                                    180
120
                                                                                                                          ----tsghhhh 213
                                                                                                                                                                                                                                                                                 gene; Nef protein; Tat protein;
         QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                   FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                            COVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV Tat or Nef protein linked to a fusion partner
                                                                                                                                                                                                                                                              A representative LipoD-Nef-His fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                 fusion protein; HIV nef infection; protein D.
                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                         AAY02352 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Marchand M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                         98WO-EP06040
                                                                                                                                                                                                                                                                                                                                                                                          97GB-0020585.
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Godart SAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-302282/25.
N-PSDB; AAX35688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                                                                HIV nef gene;
                                                                                                                                                                                                                                                                                                                                      W09916884-A1
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                                                                                                                                                        11
hh 215
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                                                                                                                                           301 HH 302
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                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bruck C,
                                                                                                                                                                                                                          AAY02352;
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61
                 61
                                  121
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The present sequence represents a His-tagged Nef protein of HIV, with a lighdation signal sequence (LipoD) which is removed after processing. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat; and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The
                                                                             289
                                                                                                           181 LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSOPKTACTNCYCKKCCFH 240
                                                                                                                                                                                              New use of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef linked to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 protein or polynucleotide for the manufacture of a vaccine -
FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                            241 COVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; nef gene; tat gene; vaccine; gpl20 gene; HIV viral load.
                                                                                                                                Amino acid sequence of a His tagged LipD-Nef of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.109
/note= "ProtD fusion partner"
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                                                                                                                                                                                                                                                                                                                                                         AAG63234 standard; Protein; 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2000; 2000GB-0002200.
14-APR-2000; 2000GB-0009336.
06-JUN-2000; 2000GB-0013806.
28-JUN-2000; 2000WO-EP05998.
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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87; Gaps

Indels

Length 324;

DB 20; 0

Score 1139.5; DB 20 Pred. No. 2.2e-102;

Query Match 67.5%; Best Local Similarity 71.2%; Matches 215; Conservative

0; Mismatches

9

1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA

ò g 1;

Gaps 9

Indels

DB 20; Length 326;

180

291

231

171

317

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QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                               241 CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH 300
                                                                                                             LEWREDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH
                                                                                                                                                                                                FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                                                                                                                                                            lewrfdsrlafhhvarelhpeyfknc------
the invention. The specification also describes fusion proteins comprising HIV-1 Tat protein. The fusion protein can be used in vaccine to prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a His tagged ProtD-Nef fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tat gene; vaccine; gpl20 gene; HIV viral load
                                                                      Score 1139.5; DB 20
Pred. No. 2.2e-102;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..111
/note= "ProtD fusion partner"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                                                                                                                                                                                                                                                                                                             AAG63236 standard; Protein; 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus.
                                                                      67.5%;
llarity 71.2%;
Conservative
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2000GB-0013806
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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N-PSDB; AAH42880.
                                                                                 Best Local Similarity
Matches 215; Conser
                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; nef gene;
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                                         326
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| hh 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2001
                                                                                                                                                                                                                                                                                                                        301 HH 302
                                                                                                                                                                                                                                                                                                     318 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                  AAG63236;
                                            Sequence
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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 HIV viral load in HIV infected humans and results CD4+ levels over those levels found in the absence HIV Tat, Nef or Nef-Tat and HIV gp120.
                                                                                                              289
                                                                                                                                                                                                                                         LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCCFH 240
                                                                                                                                                                                                                                                                                             |||||||
-----tsghhhh 322
                                                                                                                                                         QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; Nef protein; Tat protein;
                                                                                             Gaps
                                                                                                                                                                                                            CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                         DB 22; Length 324;
                                                                                            Indels
                                                                                                                                                                                                                                                    HIV Tat or Nef protein linked to a fusion partner
                                                                        67.5%; Score 1139.5; DB 22
71.2%; Pred. No. 2.2e-102;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A representative LipoD-Nef fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jene; fusion protein; HIV nef
HIV infection; protein D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type
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                                                                                                                                                                                                                                                                                                                                                                                              AAY02354 standard; Protein; 326
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                                                                                  Best Local Similarity 71.2
Matches 215; Conservative
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 vaccine reduces the in a maintenance of of vaccination with
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N-PSDB; AAX35690.
                                           AA;
                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nef gene;
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                                                                         Query Match
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WPI; 2000-038789/03
                                        Schott M,
        (SCHO/)
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                                                                 The present sequence represents a His-tagged ProtD-Nef fusion protein. The protein is expressed in Escherichia coli, and is used to produce the vaccine of the invention. The specification describes the use of HIV Tat, HIV Nef, or Nef-Tat, and HIV gpl20 in the manufacture of a vaccine. The vaccine is used for the prophylactic or therapeutic immunization of humans against HIV. Tat, Nef or Nef-Tat act in synergy with gpl20 in the treatment and prevention of HIV. The vaccine reduces the HIV viral load in HIV infected humans and results in a maintenance of CD4+ levels over those levels found in the absence of vaccination with HIV Tat, Nef or Nef-Tat and HIV gpl20.
                                                                                                                                                                                                                                                                                                                                                FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                          QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                              231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----tsghhhh 324
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEF protein; calmodulin; negative factor protein; binding inhibitor; diagnosis; detection; infection; treatment; HIV.
       of a human immunodeficiency virus (HIV) Tat, or Nef, or Nef to Tat (Nef-Tat) protein or polynucleotide and an HIV gpl20 or polynucleotide for the manufacture of a vaccine -
                                                                                                                                                                                                                                                              1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                   292 lewrfdsrlafhhvarelhpeyfknc-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    CQVCFITKALGISYGRKKRRQRRRPPQGSQTHQVSLSKQPTSQSRGDPTGPKETSGHHHH
                                                                                                                                                                                                                     DB 22; Length 326;
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0
                                                                                                                                                                                                                                 2.2e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein/calmodulin binding inhibitor.
                                                                                                                                                                                                                    67.5%; Score 1139.5; 71.2%; Pred. No. 2.2e
                                                                                                                                                                                                                                          0; Mismatches
New use of a human immunodeficiency virus
linked to Tat (Nef-Tat) protein as ---
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                                              Disclosure; Fig 1; 90pp; English.
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es 215; Conserv
                                                                                                                                                                                     326 AA;
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Best Local S:
Matches 215
                                                                                                                                                                                      Sequence
                           protein
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                                                                                          This invention describes novel binding partners (A) (1) for negative factor protein (Nef) that competitively inhibit binding of calmodulin (I) to Nef, or (ii) for (I) that competitively inhibit binding of Nef to (I). (A) are used for prevention, diagnosis (by specific detection of intraand/or extra-callular Nef, including staging of infection), and/or treatment of infections with human immune deficiency virus (HIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSORRODILDLWIYHTOGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention and diagnosis of human
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                                                                                                                                                                                                                                                                Montagnier L;
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                                                                                                                                                                                                                                                                                                Length 206;
                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                            Score 1120; DB 21;
Pred. No. 9.3e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Granier C,
JM;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Sabatier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding agents used for treatment, immune deficiency virus infection
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                                                                                                                                                                                                                                                                                            66.4%;
99.0%;
                                                           Claim 3; Fig 1; 29pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR38893 standard; Protein;
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91US-0754300.
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Rietschoten JV, Rochat H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.0 Matches 204; Conservative
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(INSP ) INST
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04-SEP-1991;
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Best Local S
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                                                                                                                                                                                                                                   Sequence
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Gaps

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Length 206; Indels

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This invention describes a novel retroviral packing cell (I), comprising the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCWO coding gene gp, or a part of these. The products of the invention have anti-HIV and cytostatic activity and be used for gene therapy. (I) is useful for in vitro infection of cells, especially hematopoletic stem cells, for expression of transgenes in cells and as a pharmaceutical carrier for gene therapy. (I) is therefore useful in the treatment of infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and other diseases. This sequence represents the Human immunodeficiency virus (HIV-1) nef protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                    Lentivirus antigenic compositions - containing lentivirus with nef
gene deletion
                                                                                                                                                                                                                                                                                                                                                                                                   1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigenic composition; primate; lentivirus; nef gene; vaccine; infection; AIDS; HIV-1; nef protein.
                                                                                                                                                                                                                                                                                                                          Score 1115; DB 21;
Pred. No. 2.8e-100;
1; Mismatches 3;
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                                  Disclosure; Page 48; 69pp; German.
                                                                                                                                                                                                                                                                                                                                66.1%;
98.1%;
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90US-0551945.
91US-0727494.
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N-PSDB; AAV81866.
                                                                                                                                                                                                                                                                          206 AA;
and glycoproteins
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                                                                                                                    The nef protein comprises peptides which are expressed in vivo in HIV infected patients before detectable amts. of p25, gpl10 and gp41 are expressed. Thus, they can be used in assays for early detection of HIV. They can also be used to raise antibodies for use in detection, to induce cellular immunity or to raise neutralising antibodies that either inactivate the AIDS virus or reduce the viability of the virus in vivo or destroy infected cells. The peptides may be used in viral vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma; nef protein.
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                                    Diagnosis of HIV infection – by detecting HIV antibodies using antigenic polypeptide derived from nef protein of HIV-1
                                                                                                                                                                                                                                                                                                                                                 Length 206;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match 66.1%; Score 1116; DB 14; Best Local Similarity 99.0%; Pred. No. 2.3e-100; Matches 204; Conservative 0; Mismatches 2;
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N-PSDB; AAA40298, AAB10053, AAB10054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                            Disclosure; Fig 2; 15pp; English.
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   WPI; 1993-213434/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV-1 nef protein.
                                                                                                                                                                                                                                                                                               206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000
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                                                                                                                                                                                                                                                                                                 Sequence
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                          an isolated
                      The invention relates to an antigenic composition comprising an isolated primate lentivirus whose genome contains an engineered non-revertible null mutation in the nef gene, or an infectious DNA clone in a carrier. The antigenic composition is used in vaccines against infection by the lentivirus, e.g. AIDS.
                                                                                                                                                                      120
                                                                                                                                                                                180
                                                                                                                                                                                                                  A comparison of AAN60287 with the CDNA of the HTLV-III genome revealed one particular clone, designated p7.11 which contained a DNA sequence encoding this peptide (AAP60308) sequence. This approx. 2.2 kilobase covers the precursor gag region and encodes, 5' to 3',
                                                                                                                      Gaps
                                                                                                                                                     9
                                                                                                                                     1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                             QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY
                                                                                                                                                                                                        FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide(s) - obtd. by diagnosis and in vaccines
                                                                                                   Length 206;
                                                                                                                     Indels
                                                                                                  Score 1114; DB 20;
Pred. No. 3.5e-100;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome
used for
        Disclosure; Fig 2A-R; 93pp; English.
                                                                                                                                                                                                                                                   LEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                      Z
                                                                                                                                                                                                                                                                                                                                                                                        HTLV-IIIB/H9 cells (ATCC CRL 8543).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; fig 2; 125pp; English.
                                                                                                   Ouery Match
Best Local Similarity 97.6%;
Matches 201; Conservative
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85US-0805069
                                                                                                                                                                                                                                                                                                                                                                                                                                           85EP-0309454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acquired immune deficiency molecular cloning etc. and
                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against virus disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1986-177602/28.
                                                                          206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lasky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN60288.
                                                                                                                                                                                                                                                                                                                                                                        LAV; AIDS;
                                                                                                                                                                                                                                                                                                                                                       Sequence of E'
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1985;
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04-DEC-1985;
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                                                                          Sequence
                                                                                                                                                                                                                                                                                   RESULT 19
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QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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                                                                                                                                                               Gaps
                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim a polypeptide which is recognised by sera of human origin contg. antibodies against the virus of lymphadenopathies (LAV) or acquired immune deficiency syndrome (AIDS). Also claimed are various peptides corresp. to the AA sequences deducible from proteins encoded by LAV DNA, defined by specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance
                                                                                                                                                                                                                             1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSVTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                           PPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV
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P, Stewart C, Danos O;
                                                                                                                                                               Indels
                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; immunoassay; HIV; HTLV-III.
p-12, p-15, p-24 a second p-15 protein, and approx. pairs 3' to the gag region (see AAN60288).
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                                                                                                                         7;
                                                                                                                    Score 1111; DB 7;
Pred. No. 7e-100;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krust B, Chamaret S, F, Alizon M, Sonigo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of LAV virus ORF F protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 216
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PASTEUR.
                                                                                                                       Query Match 65.8%;
Best Local Similarity 97.1%;
Matches 200; Conservative
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84FR-0016013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lymphadenopathy virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1986-119166/18.
N-PSDB; AAN60365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP60423 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Montagnier L,
Barre-Sinoussi
                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wain-Hobson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS (INSP ) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1985;
18-OCT-1984;
16-NOV-1984;
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                                                                                                                         Query Match
Best Local 3
                                                               Sequence
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This invention describes a novel-fusion polypeptide which comprises (a) a first polypeptide sequence of an AIDS associated E', env, or gag polypeptide that the sequence of an AIDS associated E', env, or gag second polypeptide sequence which is not an AIDS associated vitus polypeptide sequence which is not an AIDS associated vitus polypeptide are are (1) a fusion polypeptide having a charge simplex virus (HSV) gD signal peptide sequence fused in reading a rame with a polypeptide sequence other than HSV gD, (2) a nucleic acid encoding a fusion polypeptide as in (1); (3) an expression vector comprising a nucleic acid as in (2); (4) a host comprising a vector as in (3). The AIDS-associated fusion polypeptides can be used in the detection of and vaccination against viral etiological agents of AIDS. They can also be administered as a pharmaceutical agent to inhibit infection by AIDS associated retrovirus or dissemination of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                           New AIDS-associated fusion poly:peptide(s) - used for the detection of AIDS or to inhibit infection by AIDS associated retrovirus or dissemination of such retrovirus in infected individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 1mmunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                               Example 1; Fig 2A-J; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LEWRFDSRLAFHHVARELHPEYFKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04960 standard; Protein; 216
                                                                                                                                                                                                                                                                                                                                                                       64.78;
96.18;
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Capon DJ,
                      WPI; 1999-094894/08.
N-PSDB; AAV74271.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 198; Conserv
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Modified-site
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Berman PW,
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                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; acquired immunodeficiency syndrome; viral infection; envitation polypeptide; E' protein; gag protein; pol protein; P' pr gD signal peptide; detection; vaccination; etiological agent; infection inhibitor; AIDS associated retrovirus; p24; gp41.
                                                                                      ö
                                                               Length 216;
                                                                                      Indels
                                                           Score 1107; DB 7;
Pred. No. 1.8e-99;
1; Mismatches 3;
with a formula given in the specification.
                                                                                                                                                                                                                                                                                 191 lewrfdsrlafhhvarelhpgyfknc 216
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Misc-difference 11
                                                                                                                                                                                                                                                                    181 LEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lymphotropic virus type III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label- Thr, Asn
                                                                                                                                                                                                                                                                                                                                                           AAW90179 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Glu,
153
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84US-0685272.
85US-0805069.
8BUS-027568.
92US-0129009.
94US-0282857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label- Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label- Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Leu,
                                                           Query Match 65.6%;
Best Local Similarity 98.1%;
Matches 202; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       HTLV-III E' protein.
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29-SEP-1993;
29-JUL-1994;
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                         Sequence
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Gaps 9 9

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Length 206; Indels

Score 1092; DB 20; Pred. No. 4.9e-98; 1; Mismatches 7;

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The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune caponse which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytocoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, copy administrating the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human immunodeficiency virus-1 (HIV-1) iffl Nef protein. The different codon optimised nef
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                                                                                                                                                                                                                                                                                                                                                                           Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 216;
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HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.9%; Score 1011; DB 22;
83.8%; Pred. No. 4e-90;
ive 15; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 13; 84pp; English.
                                                         2000WO-US34162
                                                                                                                99US-0172442
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Best Local Similarity 83.89
Matches 181; Conservative
                                                                                                                                                                      (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                   Shiver JW, Liang X,
                                                                                                                                                                                                                                                                                            WPI; 2001-417878/44
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                                                         15-DEC-2000;
                                                                                                             17-DEC-1999;
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21-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW53113;
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This sequence represents a protein of unspecified function contained in a complete nucleotide sequence of ARV-2 derived from partial sequences of several ARV clones. The invention provides a method for construction of a sector for expression of a polypeptide in a mammalian cell, comprising a polypeptide coding sequence operably linked downstream of an enhanced promoter. The enhanced promoter comprises the human cytomegalovirus immediate early region (HCMV IEI) promoter and the first intron proximate to the 3' end of the HCMV IEI) promoter. The polypeptide can be any of the HIV recombinant polypeptides and especially HIV gpl20. Expression of HIV gpl20 by CoS 7 cells transfected with pCMMs containing the gpl20 coding region, where pCMMs is a vector containing the above enhanced promoter, is increased by a factor of 50-100 compared with the use of a vector containing the use of a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 TOGYFPDWONYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                      cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 210;
                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                               Rosenberg
                                                                                                                                                                                                                                                                                                                                                                      Enhanced promoter for gene expression - comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.1%; Score 997; DB 19;
85.2%; Pred. No. 8.9e-89;
ive 16; Mismatches 11;
                                                                                                                                                                                                                                                                                               Luciw PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 EREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                     immediate early promoter plus intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                               Haigwood NL,
                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4C-P; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY77299 standard; Protein; 210 AA
                                                                                                                                             84US-0667501.
85US-0696534.
85US-0773447.
92US-0931191.
93US-0083391.
                                                                                                  94US-0288336
                                                                                                                               87US-0138894
                                                                                                                                                                                                                                   94US-0288336
                                                                                                                                                                                                                       93US-0107377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 85.2
Matches 179; Conservative
                                                                                                                                                                                                                                                                                               Dina D,
                                                                                                                                                                                                                                                                                                                                          WPI; 1998-007982/01.
                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 AA;
                                                                                                  10-AUG-1994;
                                                                                                                                                                                                                                                                                             Chapman BS,
                                         US5688688-A.
                                                                                                                                                                                                                                   10-AUG-1994
                                                                      18-NOV-1997
                                                                                                                                                            30-JAN-1985
                                                                                                                                                                                         17-AUG-1992
                                                                                                                                                                                                      28-JUN-1993
                                                                                                                               24-DEC-1987
                                                                                                                                                                            06-SEP-1985
                                                                                                                                                                                                                       17-AUG-1993
                                                                                                                                                                                                                                                                                                              Thayer RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
AAY77299
ID AAY7
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AC AAY7
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AAY77299

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with Ala"
Misc-difference 174.-175
/note- "Wild type dileucine motif (Leu-Leu) substituted
                                                                                                                                                                   DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; jrfl Nef; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAA 50
                                                                                                                                   HIV-1 jrfl Nef (G2A, LLAA) mutant protein.
                                                                                                                                                                                                                                   immunodeficiency virus type 1.
                                 AAE04962 standard; Protein; 217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-2000; 2000WO-US34162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shiver JW, Liang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-417878/44.
                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200143693-A2
                                                                                                   10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2001.
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                  AAE04962;
                                                                                                                                                                                                                                   Human
                   AAE04962
                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the improvement of HIV-1 immunoassays by the use of an HIV-1 antigen comprising an immunogenic fragment of recombinant or synthetic HIV-1 pol, which is encoded by an approximately 9.7 kb sequence between a BatXI restriction site at position 3006 and an NdeI site at position 5131 of the genome (the proviral DNA sequence is given in AAZ90201). The immunogenic pol fragment is not immunologically cross reactive with human T cell lymphotropic viruses I or II. The invention also encompasses the used of p31 as an antigen. The recombinant antigen may be produced in Escherichia coli, Saccharomyces cerevisiae or in mammalian cells. Immunoassays using the recombinant HIV proteins may be used to diagnose and stage HIV-1 infections. Sequences
                                                                immunoassay; antigen; pol fragment; p31; recombinant; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoassay for antibodies against human immune deficiency virus, for diagnosing infection, uses an immunogenic fragment of the pol protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 IQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggyfpdwqnytpgpgirypltfgwcfklvpvepekveeanegennsllhpmslhgmeda 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGGKWSKSSVVGWPTVRERMR----RAEPAADGVGAASRDLEKHGAITSSNTAATNAACA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.1%; Score 997; DB 21; Length 210; Best Local Similarity 85.2%; Pred. No. 8.9e-89; Matches 179; Conservative 16; Mismatches 11; Indels
                                                                                                                Human immunodeficiency virus type 1 'ATCC CRL 8597'.
                               HIV-1 (ATCC CRL 8597) ORF #3-encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 40-P; 99pp; English.
                                                                                                                                                                                                                                            93US-0089407.
87US-0138894.
92US-0931154.
84US-0667501.
85US-0696534.
                                                                                                                                                                                                                95US-0443434
                                                                                                                                                                                                                                                                                                                                  85US-0773447
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-170256/15.
N-PSDB; AAZ90201.
                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                   Luciw PA, Dina D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 AA;
                                                                                                                                                                                                                17-MAY-1995;
                                                                                                                                                                                                                                                                                                                                  06-SEP-1985;
22-MAY-2000
                                                                                                                                                                                                                                                                                               31-OCT-1984;
30-JAN-1985;
                                                                                                                                               US6013432-A
                                                                                                                                                                               11-JAN-2000
                                                                                                                                                                                                                                                08-JUL-1993
                                                                                                                                                                                                                                                               24-DEC-1987
17-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRL 8597).
                                                                              detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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99US-0172442

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'note" "Wild type myristylation site at Gly2 substituted

Location/Qualiflers 2

(first entry)

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The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The Nef protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) cresponse against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individuals, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human immunodeficiency virus-1 (HIV-1) jrfl Nef (GZA, LLAA) mutant protein. The different nef
                                                                           Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virus-1 (HIV-1) Jrfl Nef (G2A, LLAA) mutant protein. The different nef constructs of the invention are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%; Score 996; DB 22; 82.0%; Pred. No. 1.2e-88; ive 16; Mismatches 13;
                                                                                                                                                                                                                                                                                                               Claim 29; Page 18; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.07
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA;
N-PSDB; AAD09605
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us-09-509-239-13.rag

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Human tPA leader peptide-HIV-1 jrfl Nef (opt tpanef) mutant protein.
                                                                                                                                         DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HI cell mediated immune response; Cytoxixc T lymphocyte; CTL; human immunodeficiency virus-1; HIV-1; human; jrfl Nef; opt tpanef; rissue plasminogen activator; tPA; chimeric protein; mutent; mutein.
                                                                                                                                                                                      Chimeric - Human immunodeficiency virus type 1.
Chimeric - Homo sapiens.
                   PEREVLEWRFDSRLAFHHVARELHPEYFKNC
                                                                      AAE04961 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                          15-DEC-2000; 2000WO-US34162
                                                                                                        10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                        WO200143693-A2
                                                                                                                                                                                                                                                                                                                                                           17-DEC-1999;
                                                                                                                                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                               Shiver JW,
                                                                                       AAE04961;
                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
         176
                                                     27
                                                   RESULT AAE04961
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                                  DLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSL 170
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain of HIV-1 retrovirus, OYI. This mutant retroviral strain is useful in an assay for diagnosing HIV infection. See also AAQ11943 (OYI nucleotide sequence), AAR12255-61 (other HIV OYI constituent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMRRA-----EPAADGVGAASRDLEKHGAITSSNTAATNAAC
TNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDIL
                                                                                                                                                                                                                                                                                                                                                                                             Purified human retrovirus - is mutant of HIV-1 having characteristics of HIV-1 OXI, used in diagnosis of HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence constitutes the ORF F protein constituent of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                           Brun-Vezinet
                                                                                                                                                                                                               HIV-1 strain OYI open reading frame (ORF) F protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 983; DB 12;
Pred. No. 2e-87;
2; Mismatches 9;
                                                                                                         171 HGMDDPEREVLEWRFDSRLAFHHVARELHPEYFKNCT 207
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                                                                                                                                                                                                                                                                                                                                                          Delaporte
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; fig 8; 23pp; English.
                                                                                                                                                           AAR12262 standard; Protein; 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%;
ilarity 82.5%;
Conservative 22
                                                                                                                                                                                                                                                                                                                        87US-0113655.
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                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                 HIV-1; AIDS; retroviruses
                                                                                                                                                                                                                                                                                                                                                           Wain-Hobson S, Huet T,
                                                                                                                                                                                                                                                                                                                                          (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-177518/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 AA;
                                                                                                                                                                                                                                                                                                       28-OCT-1987;
                                                                                                                                                                                                                                                                                                                         28-OCT-1987;
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                   US5019510-A
                                                                                                                                                                                              20-AUG-1991
                                                                                                                                                                                                                                                                                     28-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                             AAR12262;
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                                                                                                                181
                                           61
                                                            111
                          51
                                                                                                                                        RESULT 2
AAR12262
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1..26 /label= Leader\_peptide /note= "Human tissue plasminogen activator (tPA) leader sequence"

Location/Qualifiers

27..237 // Anture HIV-1 Nef (6-216aa) protein" 195..196

/label- Dileucine\_motif

99US-0172442

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Liang X,

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The present invention relates to a DNA vaccine comprising a DNA expression vector, and a DNA molecule containing a codon optimised open reading frame encoding a Net protein or its immunogenic derivative. The Net protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) response against infection or disease caused by virulent strains of HIV, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, preferably human. It is also useful for lowering transmission rate to previously unifected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human tissue plasminogen action and the myristylation site (G1y2) in the HIV-1 jifl Nef (opt thanef) chimeric mutant protein. The mutation include deletion of the myristylation site (G1y2) in the HIV-1 jifl Nef protein. The different codon optimised nef constructs of the invention are used
                                                                                                                                                                         Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Page 17; 84pp; English.
WPI; 2001-417878/44.
                                                        N-PSDB; AAD09604.
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56 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 115 

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HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 175

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Hahn BH, Shaw GM, Gao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69363;
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
AAB69363
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with Ala-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel DNA vaccine useful for inducing cell mediated immune response against virulent strains of HIV, comprises DNA expression vector, and DNA containing codon optimized open reading frame encoding Nef protein
                                                                                                                                                                                                                                                                                                                     DNA vaccine; codon optimisation; Nef protein; HIV infection; anti-HIV; cell mediated immune response; cytotoxic T lymphocyte; CTL; human immunodeficiency virtus-1; HIV-1; human; irfl nef; opt tpanef; tissue plasminogen activator; tPA; chimeric protein; mutein.
                                                                                                                         AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 115
                                                                                                                                                  HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 175
                                                                                      10; Gaps
                                                                             6 SKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAATNAAC 55
                                                                                                                                                                                                                                                                                                                                                                                                  1..26
/label- Leader_peptide
/note- "Human tissue plasminogen activator (tPA)
leader_sequence"
                                                                                                                                                                                                                                                                                                    Human tPA leader peptide-HIV-1 jrfl Nef (LLAA) mutant protein.
                                            Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                   27 237
/note= "Mature HIV-1 Nef (6-216aa) protein"
                                                             Indels
                                           ; Score 978; DB 22;
; Pred. No., 7.4e-87;
15; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
                                                                                                                                                                                    176 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
in the exemplification of the invention.
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                AAE04963 standard; Protein; 237
                                           57.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0172442
                                                   ilarity 83.4%;
Conservative
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-417878/44.
N-PSDB; AAD09606.
                                           Query Match
Best Local Similarity
Matches 176; Conserv
                 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200143693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                               Chimeric
Chimeric
                                                                                                                                                                                                                                                                  AAE04963;
                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                               RESULT 28
                                                                                                                                                 116
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the procession vector, and a DNA molecule containing a codon optimised open reading frame encoding a Nef protein or its immunogenic derivative. The protein or its derivative is expressed and generates an immune response which provides a substantial level of protection against HIV infection, upon administration of to a host. The DNA vaccine is useful for inducing a cell mediated immune (cytotoxic T lymphocyte, CTL) by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate host, by administering the DNA vaccine into the tissue of the vertebrate to previously uninfected individuals and/or for reducing levels of viral loads within an infected individual, so as to prolong the asymptomatic phase of HIV infection. The present sequence is human tissue plasminogen activator (tPA) leader peptide human immunodeficiency virus-1 (HIV-1) if Nef (LLAA) chimeric mutant protein. The different codon optimised nef constructs of the invention are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 HTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 SKSSVVGWPTVRERMRRAEPAAD------GVGAASRDLEKHGAITSSNTAATNAAC
                                                                         The present invention relates to a DNA vaccine comprising a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length .237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%; Score 968; DB 22; Length.23
82.5%; Pred. No. 7e-86;
iive 15; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV-1 non-subtype B clone 962M651-8 nef protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 PEREVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'pu; vif; vpr; tat; rev; nef; vaccine.
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Claim 29; Page 19; 84pp; English.
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Matches 174; Conservative
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2001-336417/36

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Search completed: August 26, 2002, 08:12:25
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                                                                                           The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV
                                                                                                                                                                                                                                                                                                                                                                                                  61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
                                                                                                                                                                                                                                                                                                                                                                                       121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
                                                                                                                                                                                                                                                                                                               9
                    Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific nucleotide sequence
                                                                                                                                                                                                                                                                                        1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA
                                                                                                                                                                                                                                                                                                     61 geeeevgfpvrpqvplrpmtykaavdlsfflkekgglegliyskkrgeildlwvyhtggf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection; diagnosis; human; humoral immune response; antiviral; cellular immune response; vaccine; treatment; gene therapy.
                                                                                                                                                                                                                                           Length 206;
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(GENE-) GENEART GMBH GES ANGEWANDIE BIOTECHNOLOG.
                                                                                                                                                                                                                                          56.4%; Score 952; DB 21;
llarity 81.1%; Pred. No. 2.1e-84;
Conservative 24; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB86169 standard; Protein; 3025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1 subtype C protein fragment #1.
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1..3025
/label= Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type
                                                                     Claim 41; Fig 22; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LEWRFDSRLAFHHVARELHPEYFKNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2000; 2000DE-1056747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
WPI; 2000-365651/31
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                                                                                                                                                                                                                                                      Best Local Similarity
Matches 167; Conserv
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Misc-difference
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This invention describes a novel polynucleotide isolated from human immunodeficiency virus type I subtype C/B' which can be used for the induction of specific humoral and cellular immune responses. (I) and coloded by them, are useful in pharmaceuticals.

To polypeptides (II) encoded by them, are useful in pharmaceuticals.

To human immune deficiency virus; particularly for treatment or prevention of human immune deficiency virus; particularly for treatment or prevention of human immune deficiency virus; (HIV-1) infections, also for rational design of test or therapeutic respents, or gene therapy vectors.

To Polypeptides, specially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents (II) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in the method of the invention.
                                                                                                          New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 8A-O; 48pp; German.
N-PSDB; AAH20870
                                                                                                                                                                                                                                                     infection
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2723 mggkwsksslvgwpairermrrtepaadgvgavsrdlekhgaitssntaatnedcawlea 2782 |:|:|||:|| | |||||||::|:| 2903 lkwkfdsq1ahrhrarelhpefykdcxhrrdfprglstgafxevws--ggtgsgqpsnaa 2960 9 1 MGCKWSKSSVVGWPTVRERMRREPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 181 LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPR-----LEPWKHPGSQPKTACTNCY Length 3025; Indels DB 22; 56.2%; Score 948.5; DB 22; llarity 70.6%; Pred. No. 1.9e-82; Conservative 22; Mismatches 42; Best Local Similarity Matches 175; Conserv 2961 ykqllfac 2968 234 CKKCCFHC 241 Query Match

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3025 AA;

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Sequence 43,
Sequence 1, A
Sequence 1, A
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Sequence 15,
Sequence 4,
Sequence 4,
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                                                                                                                                                                                                                                                                                                          1 MGGKWSKSSVVGWPTVRERM.....QSRGDPTGPKETSGHHHHH
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-679-493A-75
US-08-679-493A-74
US-08-450-257-1
US-08-450-098-1
US-08-451-233-1
US-08-451-233-1
US-07-808-451-233-1
US-07-808-452-1
US-07-808-452-1
US-07-808-452-1
US-09-030-613-19
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PCT-US95-06077-2
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US-09-256-490-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    - protein search, using sw model
                                                                                                                                                     August 26, 2002, 08:08:31
                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
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1688
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Match
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                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Maximum DB
                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
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Sequence 4, Appli Sequence 17, Appl Sequence 17, Appl	1, 1 1, 1 27,	27, 27, 27,	Patent No. 5223423 Sequence 2, Appli Sequence 5, Appli Sequence 3, Appli Sequence 1, Appli	Sequence 48, Appl Sequence 7, Appli
5 PCT-US96-11445-4 3 US-09-030-613-17 1 US-09-451-905-17	2 US-08-893-853-1 1 US-09-113-921-1 5 5304466-3 1 US-08-094-128A-27	1 US-08-455-674-27 1 US-08-455-992-27 1 US-08-455-972-27 5 PCT-US92-00652-27	5 5223423-3 1 US-07-910-867B-2 1 US-07-910-867B-5 1 US-07-910-867B-3 1 US-07-910-867B-1	1 US-09-055-075C-48 1 US-08-450-257-7
253	72 72 72 72 4 122 6 8 312 1	312	3025 72 72 72 72 72	56.
25.5 24.2	22.8 22.8 22.0 21.7	21.7 21.7 21.7	221 200.9 199.6 189.3	17.2
430.5	385 385 372 365.5	2000 2000 2000 2000 2000 2000 2000	362.5 352 331 325 311	290
9008	337 337 34	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	24444 2015 E	4 4 5

## ALIGNMENTS

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61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LEWRFDSRLAFHHVARELHPEYFKNCTSEPVDPRLEPWKHPGSQPKTACTNCYCKKCC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR RPLING DATE: 1995-09-01
PRIOR PELING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PATENTING DAYE: 2.0
SOFTWARE: PATENTING DAYE: 2.0
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Pred. No. 1.2e-108;
2; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(239)
COTHER INFORMATION: X os selenocysteine.
US-08-679-493A-76
                      ; Sequence 76, Application US/08679493A
; Patent No. 6303295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
US-08-679-493A-76
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RESULT 2 US-08-388-353-644

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121 FPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75, Application US/08679493A
Sequence 75, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W
TITLE OF INVENTION:
FILE REFERENCE: 55-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
                                                                                                                                                                                                                                                                           UVERMILIUS SISIEMI: PC-LUOS/MS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995.
PRIOR APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATION DATE: 17-MAY-1995
ATION NUMBER: NUMBER: DN3021/95
FILING DATE: 17-MAY-1995
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1 NUMBER OF SEQUENCES: 841 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 1115; DB 3; 98.1%; Pred. No. 2.1e-106; iive 1; Mismatches 3;
                                                                E: SCULLY, SCOTT, MURPHY & PRESSER 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LEWRFDSRLAFHHVARELHPEYFKNC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: FRANK S. DIGIGLIO REFERENCE/DOCKET NUMBER: 9606Z TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.1
Best Local Similarity 98.1
Matches 202; Conservative
                                                                                                                                                                           ZIP: 11530-0299
COMPUTER READABLE FORM:
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                                                                                                                                                           COUNTRY:
                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                           APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Morbhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1115; DB 3;
Pred. No. 2.1e-106;
                                                                                                                                                                                                                                                  ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/388,353
14-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 644, Application US/08388353 Patent No. 6010895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
REPERCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELESX: (530 901 SANS UR
INFORMATION FOR SEQ ID NO: 644:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicholas J. Deacon
Dale A. McPhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 98.1%;
Matches 202; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acid
                                                                                                                                                                                                                                                                                                                  New York
United States
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                         Garden City
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APPLICANT: Nichola
APPLICANT: Dale A.
APPLICANT: David C
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US-08-488-551B-644
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Mismatches
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; OTHER INFORMATION: X is selenocysteine.
US-08-679-493A-74
                                                                                                                                                                                                                                                                                     Sequence 74, Application US/08679493A Patent No. 6303295 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08450257; Patent No. 5652122; GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 LEGL--IHSQRRQDI-LDLWI 114
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SOFTWARE: PatentIn Ver. 2.0
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Matches 103; Conservative
      Conservative
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ADDRESSEE: FISH & NE
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                                                                                                                                                                                         121 FPD 123
                                                                                                                                                                                                                                                        RESULT 6
US-08-679-493A-74
     120,
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US-08-450-257-1
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SEQ ID NO 74
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGG---LEGLIHSQRRQDILDLWIYHT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 QGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDFE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                                                                                                                                                                                                                                                                                        ;
6
                                                                                                                                                                                                                                                                                                                     Length 206;
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                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                 Score 971; DB 4; L
Pred. No. 1.2e-91;
2; Mismatches 15;
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Pred. No. 7.3e-58;
                                                                                                                                                                                     ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human imunodeficiency virus type
CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT FILING DATE: 1996-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/EP95/01481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HIV-Vaccines
FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 REVLEWRFDSRLAFHHVARELHPEYFKNC 206
                                                                                                                                                                                                                   NAME/KEY: VARIANT
COTATION: (1)..(206)
CHER INFORMATION: X is selenocysteine.
US-08-679-493A-75
                             PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09124900 Patent No. 6268484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHMATZ, Christine
KLIMA, Annelies
STEINDL, Franz
MUSTER, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1995-04-19
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97.6%;
                                                                                                                                                                                                                                                                                                                     57.5%;
89.0%;
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ERNST, Wolfgang
BALLAUN, Claudia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PURTSCHER, Martin
TRKOLA, Alexandra
PREDL, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KATINGER, Hermann
                                                                                                                                                                                                                                                                                                                     Query Match 57.5
Best Local Similarity 89.0
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
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Best Local Similarity
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61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKRKGGTGRANSLPTKTRYPXSVDLPHTRL 120
                                                                                                                                                                                      61 QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLMIYHTGGY 120
                                                                                                                                                         QEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGY 120
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Gaps
                                                   1 MGGKWSKSSVVGWPTVRERMRRAEPAADGVGAASRDLEKHGAITSSNTAATNAACAWLEA 60
                                                                                  APPLICANT: TAYLOR, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
TITLE REFERENCE: 55-95
CURRENT APPLICATION UNMER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR FILING DATE: 1995-07-14
PRIOR FILING DATE: 1995-09-01
PRIOR FILING DATE: 1995-09-01
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.5%; Score 498.5; DB 4;
73.0%; Pred. No. 1.8e-43;
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209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.8%; Score 486; DB 1; Length 86; Best Local Similarity 100.0%; Pred. No. 1.6e-42; Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                    CLASSILLATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: POTY/US93/0783
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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Patent No. 5674980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PABO, Carl
BARSOUM, James G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haley Jr., James F
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANKEL, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                             STATE: New COUNTRY: US ZIP: 10020
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-450-246-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAT-DERIVED TRANSPORT POLYPEPTIDES
                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.8%; Score 486; DB 1; I
100.0%; Pred. No. 1.6e-42;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APPL
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-AN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATYONREY/AGENT INPORMATION:
NAME: Haley Jr., James F.
REGERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
FELENCOMMUNICATION INFORMATION:
1251 Avenue of the Americas
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/450,257
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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Conservative 0;
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APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 86 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 85; Conserv
                                           New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                          10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-450-257-1
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Gaps

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209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                         AFFLICANT: FAWELL, Stephen ...
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
TITLE OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH 6 NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                  STATE:
CONTRY: USA
2 19 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY 1995
FILING DATE: 25-MAY 1995
FILING DATE: 25-MAY 1995
FILING DATE: 25-MAY 1995
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CLASSIFICATION: 514
PRIOR PAPE: 25.MAY 1995
CLASSIFICATION: 514
PRIOR PAPE: 28.MAY 1995
FILING DATE: 28.APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21.AUG-1993
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28.JUL-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19.AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21.DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21.ABC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 21.ABC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: APPLICATION NUMBER: US 07/636,662
FILING DATE: APPLICATION NUMBER: US 08/158,015
FILING DATE: AL-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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REFERENCE/DOCKET NUMBER: B170
TELECOMMUNICATION INFORMATION:
                                                                                                                                   PABO, Carl
BARSOUM, James G.
FAWELL, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELES: 14-8367
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type 1
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US-08-450-236-1
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APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10020
COMPINEN: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 86;
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                                                                                                                                                                                                                                                                                                                                                                    CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATA:
COMPUTER: IBM PC COMPATA:
COMPUTER: IBM PC COMPATA:
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 28-MAY 1995
CLASSIFICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-APR-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-ADR-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION NUMBER: 27,794
REGISTRATION NUMBER: 28-9000
TELESTAR: (212) 596-9000
TELESTAR: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus
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; Sequence 1, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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Patent No. 6083706
GENERAL INFORMATION:
APPLICANT: FLOR'SEWICZ, Robert Z.
APPLICANT: Baird, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
CLASSIFICATION: 514
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100.0%; Pred. No. 1.6e-42;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                 STREET: Job Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                       Sequence 1, Application US/07808452
Patent No. 6663612
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Base
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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REGISTATION UNDRER: 33,875
REFERENCE/DOCKET UNMER: 8255
RECCOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0800
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 86 amino acids
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Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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                                                      US-07-808-452-1
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                                                                          APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PENINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT: POLYPEPTIDES
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: 28-AR-1994
PILING DATE: 28-AR-1994
PILING DATE: 21-AR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/454,60
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTONNEY,AGGNT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 37,794
REFERENCE/DOCKET NUMBER: 37,794
REFERENCE/DOCKET NUMBER: BTTO CIP 2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
Sequence 1, Application US/08450236
Patent No. 5804604
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Conservative 0
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TELEX: 14-8367
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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Matches 85; Conserv
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New York
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209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRQRRRPPQG 61
                                                                                                                         2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPGG 61
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Robert Z. Florkiewicz
APPLICANT: Robert Z. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME
FILE REPERENCE: 200124 402C4
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 486; DB 4; Length 86;
Pred. No. 1.6e-42;
0; Mismatches 0; Indels
             Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: FAWELL, Stephen E.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEFINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
           28.8%; Score 486; DB 4; 100.0%; Pred. No. 1.6e-42; 1ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 Avenue of the Americas
                                                                                                                                                                                          269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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                                                                                                                                                                                                                 62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09451905
Patent No. 6306613
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28.8%; Sc
Best Local Similarity 100.0%; P
Matches 85; Conservative 0;
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Query Match
Best Local Similarity 100.0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Homo sapien
US-09-451-905-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-451-905-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
US-08-235-403-1
                                                                                                                                                                                                                                                                                                                                                                       ; Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 86;
                                                                                                                                                                              CURRENT APPLICATION Belease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,613
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORREY/AGENT INFORMATION:
NAME: NO. 6083706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 39,317
REFERENCE/COCKET NUMBER: 30,317
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 19:
SEQUENCE CHRRACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; L
1.6e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.8%; Score 486; DB
100.0%; Pred. No. 1.6
Live 0; Mismatches
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1995-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE OF PREFRENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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PRIOR FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 6
LENGTH: 86
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PURTSCHER, Martin
TRKOLA, Alexandra
PREDL, Renate
SCHMATZ, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KATINGER, Hermann
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STEINDL, Franz
MUSTER, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 85; Conservative
           Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                            98104
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APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.8%; Score 486; DB 5; Length 86; 100.0%; Pred. No. 1.6e-42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the sequence of the TAT protein of {\tt HIV-1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Howson and Howson
1: Spring House Corporate Cntr, PO Box 457
Spring House
: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version, #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,215
REFERENCE/COCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
REPERENCE/DOCKET NUMBER: P-29(
TELECOMMUNICATION INFORMATION:
TELEPHAN: (415) 859-4550
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 aniho acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.85
Best Local Similarity 100.0
Matches 85; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
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; INDIVIDUAL ISOLATE:
PCT-US92-10770-1
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                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.8%; Score 486; DB 4; I
100.0%; Pred. No. 1.6e-42;
iive 0; Mismatches 0;
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                                                          PRICKATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-402-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 07/636,662
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
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APPLICATION NUMBER: PCT/US92/10770
FILING DATE: 19921211
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
TELECAMONICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
APPLICATION NUMBER: US/08/235,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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STREET: 333 Ravenswood Avenue
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                     FILING DATE:
CLASSIFICATION:
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66 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 NYTPGPGVRYPLTFGMCYKLVPM----IETV------PVKLKFGMDGP--KVKOW 252
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APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, TECTOR
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETI, ENZO
APPLICANT: PAOLETI, ENZO
APPLICANT: VECTORS STEVEN E.
APPLICANT: VECTORS HAVING ENHANCED EXPRESSION, AND
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF MAKING AND USES THEREOF
                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/816,155B FILING DATE: 12-MAR-1997 CLASSIFICATION: 514
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Pred. No. 4.8e-41;
4; Mismatches 6;
                      TITLE OF INVENTION: METHODS OF MAKING AND CORRESPONDENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE 6 HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/09079587 Patent No. 6130066 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KOMALEXI, THOMAS J.
RECISTRATION NUMBER: 32.147
REFERENCE/DOCKET NUMBER: 4543
TELECHONNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.3%;
ilarity 77.3%;
Conservative
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                                                                                                         : 745 FIFTH AVENUE
NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 92; Conserv
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STATE: NEW YORK
                                                                                                                                                      NEW YORK
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APPLICANT: TARTACLIA, James
APPLICANT: GCBEL, Scott J.
APPLICANT: GCX, William I.
APPLICANT: GCYTIG, Russell R.
APPLICANT: GETIG, Russell R.
APPLICANT: PACUES, Bertram L.
APPLICANT: PACUES, Bertram L.
TITLE OF INVENTION: VCTORS HAVING ENHANCED EXPRESSION, AND METHODS OF TITLE OF INVENTION: WAKING AND USES THEREOF
FILE REFERENCE: 454310-3010
CURRENT APPLICATION NUMBER: US/08/815,809
CURRENT FILLNG DATE: 1997-03-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                     209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                               Gaps
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4.5e-41;
6;
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100.0%; Pred. No. 1.6e-42;
iive 0; Mismatches 0;
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4; Mismatches
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Patent No. 5990091
GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
                                                                                                                                                                                                                                                                                                                                                                                          269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
                                                                                                                                                                                                                                                                                                                                                                                                                   62 SQTHQVSLSKQPTSQSRGDPTGPKE 86
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Patent No. 6004777
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COX, WILLIAM I.
GETTIG, RUSSELL R.
MARTINEZ, HECTOR
PAOLETTI, ENZO
PINCUS, STEVEN E.
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Best Local Similarity 77.3%;
Matches 92; Conservative 4
                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                              Query Match 28.8
Best Local Similarity 100.
Matches 85; Conservative
                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-06077-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Vaccinia virus
US-08-815-809-5
                                                                                         amino acid
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Length 280;

Indels

40,373

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REGISTRATION NUMBER:
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US-09-099-333-1
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                                                                                                                                                                                                                                                                                                                                       STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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APPLICANT: GUSS, Tania
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
TITLE OF INVENTION: OF VIRAL PROFEINS FOR OBTAINING AN ANTIVIRAL EFFECT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGCLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 NYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLH-GMDDPEREVLEW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 NYTPGPGVRYPLITFGMCYKLVPM----IETV------PVKLKPGMDGP--KVKQW 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: 1737 King Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.8e-41;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 478.5;
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/215,248 FILING DATE: 21.4MRT.1994 FILING DATE: 21.4MRT.1994 APPLICATION DATA: APPLICATION NUMBER: WO PCT/FR94/01457 FILING DATE: 13.DEC.1994 ATTORNEY.AGENT INFORMATION: NAME: Dadio, Susan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/505,210 FILING DATE: 14-AUG-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08505210 Patent No. 5981258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%;
ilarity 77.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: n/
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 92; Conserv
                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Itis
MOLECULE TYPE:
US-09-079-587-43
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GENERAL INFORMATION:
APPLICANT: METALI, Majid
APPLICANT: METALI, Majid
APPLICANT: METALI, Majid
APPLICANT: METALI, Majid
APPLICANT: GUSS, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL
TITLE OF INVENTION: PROTEINS FOR OBTAINING AN ANTI-VIRAL EFFECT
FILE REFERENCE: 01775-091
CURRENT APPLICATION NUMBER: US/09/099,333A
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: RP 93 14914
EARLIER APPLICATION NUMBER: RP 08/215,248
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER PILING DATE: 1994-03-21
EARLIER FILING DATE: 1995-08-14
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 EPVDPRLEPWKHPGSOPKTACTNCYCKKCCFHCOVCFITKALGISYGRKKRRQRRRPPQG 268
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                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: sequence of the TAT protein of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 470; DB 2; Length 86;
Pred. No. 7.1e-41;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
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Pred. No. 7.1e-41;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type
US-09-0393-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 SQTHQVSLSKQPTSQSRGDPTGPKE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09099333A Patent No. 6228369
REFERENCE/DOCKET NUMBER: 0177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%;
96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.8%;
Best Local Similarity 96.5%;
Matches 82; Conservative
                                                                                                                                                                                                                   ACTUDED: Jinear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORGINAL SOURCE: ORGANISM: HUMAN 1mm.r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Ver. 2.0
                                                                                                                                                              LENGIH: 86 amino acids
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                                                                                                                                                                                                              single
                                                                                                                                                                                   amino acid
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Best Local Similarity
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209 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQG 268
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Patent No. 5883081

GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Talbott, Randy
APPLICANT: Toeschia, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
INUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: 5
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EPVDPRLEPWKHPGSQPKTACTNCYCKKCCFHCQVCFITKALGISYGRKKRRQRRRPPQE 61
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,251
FILING DATE: No. 5883081 yet assigned
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-JUL-1995
ATTORNEY/AGENT INFORMATION:
COMPUTER: IBM PC compatible
COMPUTER: Hordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,079A
FILLING DATE: 26-APR-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RObinson, Joseph, R.
REFERENCE/DOCKET NUMBER: 4436/16060US4
TELECHONOUS: (212)527-7700
TELEFAX: (212)527-7700
TELEFAX: (212)527-7701
TELEFAX: (212)53-6237
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-053-079A-15
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94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                    Sequence 96, Application US/08417210A
Patent No. 5863542
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNOBEFICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/417,210A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natural Human IgM Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISCRATION NUMBER: 32 J47
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 96:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08053079A
Patent No. 506026
GENERAL INFORMATION:
APPLICANT: Rodman
TITLE OF INVENTION: Natural Human IG
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
COUTRY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 NYTPGPGVRYPLTFGWCYKLVP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.6%;
Best Local Similarity 100.0%;
Matches 82; Conservative 0
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: amino acid US-08-417-210A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 83 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New COUNTRY: U. ZIP: 10022
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                                              -08-417-210A-96
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APPLICANT: Wong-Staal, Flossie
APPLICANT: Mong-Staal, Randy
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               Length 253;
                                                                                                                                                                                                                           /note- "nef protein encoded by HIV-2KR"
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                          25.5%; Score 430.5; DB 2; 39.4%; Pred. No. 3.4e-36; Live 29; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,490
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NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,251
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; Sequence 4, Application US/09256490
; Patent No. 6235881
; GENERAL INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    Query Match 25.5%
Best Local Similarity 39.4%
Matches 99; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                     CCATION: 1.253
CTHER INFORMATION:
US-08-659-251-4
                                                                                                                                                                                  NAME/KEY: Protein
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61 QQGDFMNTPWRTPAAGREGTLYKQQNMDDVDADNDNLIGVPVTPRVPLRAMTYKLAVDIS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...---LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGASGSKKCSRSLQGLRERLLRARGETCGGQWDGSAGEYLQFQEGSGRGQNLPSCEGQRY 60
                                                                                                                                                                                                                                                                                                                                                                                                    Length 253;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor
                                                                                                                                                                                                                                                                                                                                                                                                    25.5%; Score 430.5; DB 4; 39.4%; Pred. No. 3.4e-36; live 29; Mismatches 82;
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---- 5555-399C1
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APPLICATION NUMBER: PCT/US96/11445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS9611445 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 023:
TELECOMMUICATION INFORMATION:
TELEPHONE: (415, 576-0200
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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NAME: Betliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION:
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(213) 977-1003
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                                                                                                                                                                                                                          MOLECULE TYPE: protein
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STATE: California
COUNTRY: USA
21P: 90012-2628
                                                                                                                                                                                                                                                              ; NAME/KEY: Protein
; LOCATION: 1.253
; OTHER INFORMATION:
US-09-256-490-4
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SOFTWARE: PatentI
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LEAQEEEEVGFPVTPQVPLRPMTYKAAVDLS 88
                                                                                                                                                                                                                                                                                                                           1 MGGKWSKSSVVGWPTVRERMRRAEPAADG---VGAASRDLE-KHGAITSSNTAATNAA-- 54
                                                                                                                                                                                                                                                   Length 253;
                                                                                                                                                                                 /note= "nef protein encoded by HIV-2KR"
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APPLICANT: Balrd, J. Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
WUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                     DB 5;
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                   Query Match 25.5%; Score 430.5; DB 5; Best Local Similarity 39.4%; Pred. No. 3.4e-36; Matches 99; Conservative 29; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: NO. 603706tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09030613 Patent No. 6083706 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                 LENGTH: 253 amino acids TYPE: amino acid STRANDEDNESS:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                           ) NAME/KEY: Protein
; LOCATION: 1..253
; OTHER INFORMATION:
PCT-US96-11445-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
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APPLICANT: Robert Z. Florkiewicz
APPLICANT: Andrew Baird
APPLICANT: Andrew Baird
APPLICANT: Dale E. Warnock
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING TH
FILE REFRENCE: 200124.40204
CURRENT APPLICATION NUMBER: US/09/451,905
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEO ID NOS: 48
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 409; DB 4; Length 72;
Pred. No. 9.7e-35;
0; Mismatches 0; Indels
                                                                                                                                                 Length 72;
                                                                                                                                                                                          Indels
                                                                                                                                                 Query Match 24.2%; Score 409; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 9.7e-35;
Matches 71; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; P.
Matches 71; Conservative 0;
LENGTH: 72 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien
US-09-451-905-17
                                                                                                                                                                                                                                                                                                                      269 SQTHQVSLSKQ 279
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                                                                    linear
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US-09-030-613-17
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US-09-451-905-17
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LENGTH: 72
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